GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 15:04:42 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-6
Perfect score: 15
Sequence: 1 RCTCCAYTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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96: gb_in4:*
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98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	92.0	15	9	A70378	A70378 Sequence 8
c	2	13.8	92.0	21	10	AX095547	AX095547 Sequence
c	3	13.8	92.0	160	94	MUSAIC2A09	M94144 Mus musculu
c	4	13.8	92.0	207	94	MUSIL4R07	M64874 Mouse inter
c	5	13.8	92.0	213	91	D88111	D88111 Homo sapien
c	6	13.8	92.0	248	7	ECIL7R1	AF115754 Equus cab
	7	13.8	92.0	367	54	G65440	G65440 stdJ388M5_1
c	8	13.8	92.0	403	93	HSIL7R5	AF043127 Homo sapi

c	9	13.8	92.0	490	10	I21102 I21102 Sequence 73
c	10	13.8	92.0	490	97	HUMIL2RG05 L12180 Human inter
c	11	13.8	92.0	537	14	CNS01DQR AL117163 Botrytis
c	12	13.8	92.0	572	74	AC072998 AC072998 Giardia i
c	13	13.8	92.0	585	71	AC030504 AC030504 Giardia i
c	14	13.8	92.0	652	7	AF029294 AF029294 Mustela v
c	15	13.8	92.0	681	7	AF169792 AF169792 Ursus mar
c	16	13.8	92.0	686	9	AR031381 AR031381 Sequence
c	17	13.8	92.0	693	10	I19686 I19686 Sequence 10
c	18	13.8	92.0	693	45	E09306 E09306 DNA encodin
c	19	13.8	92.0	719	7	OARNAPR Y10808 O.aries mRN
	20	13.8	92.0	735	72	AC051255 AC051255 Giardia i
c	21	13.8	92.0	759	10	I19685 I19685 Sequence 8
c	22	13.8	92.0	759	45	E09305 E09305 DNA encodin
c	23	13.8	92.0	768	95	S70302 S70302 cytokine re
c	24	13.8	92.0	770	53	CNS072TH AL426651 clone BA0
	25	13.8	92.0	807	6	EACMZ8 X12445 Eimeria ace
c	26	13.8	92.0	831	71	AC041965 AC041965 Giardia i
c	27	13.8	92.0	900	7	AF041977 AF041977 Ovis arie
c	28	13.8	92.0	931	93	HSIL5R3 X61178 Human HSIL5
	29	13.8	92.0	938	9	A70386 A70386 Sequence 16
	30	13.8	92.0	1006	7	OAPROLACR Y10578 O.aries mRN
c	31	13.8	92.0	1020	91	D88110 D88110 Homo sapien
c	32	13.8	92.0	1044	10	I19684 I19684 Sequence 6
c	33	13.8	92.0	1044	45	E09304 E09304 Human cDNA
c	34	13.8	92.0	1062	10	I19680 I19680 Sequence 1
c	35	13.8	92.0	1074	9	AR031384 AR031384 Sequence
c	36	13.8	92.0	1098	53	CNS06TDL AL414415 T3 end of
c	37	13.8	92.0	1110	10	I19683 I19683 Sequence 5
c	38	13.8	92.0	1110	45	E09303 E09303 Human cDNA
c	39	13.8	92.0	1120	8	AF222783 AF222783 Gallus ga
c	40	13.8	92.0	1188	9	AR040674 AR040674 Sequence
c	41	13.8	92.0	1188	10	E06798 E06798 DNA encodin
c	42	13.8	92.0	1188	10	I14817 I14817 Sequence 11
c	43	13.8	92.0	1205	7	CFU04361 U04361 Canis famil
c	44	13.8	92.0	1222	8	AF080247 AF080247 Tilapia m
c	45	13.8	92.0	1260	9	AR040672 AR040672 Sequence

ALIGNMENTS

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RESULT   1
A70378
LOCUS       A70378          15 bp    DNA             PAT       07-MAY-1999
DEFINITION  Sequence 8 from Patent WO9811225.
ACCESSION   A70378
VERSION     A70378.1  GI:4774659
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
            Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
            Kikuchi,Y.
  TITLE     A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
  JOURNAL   Patent: WO 9811225-A 8 19-MAR-1998;
            NICOLA NICOS ANTONY (AU)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      7 c      0 g      3 t      3 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          |||||||||||||||

Db      1 RCTCCAYTCRCTCCA 15


RESULT   2
AX095547/c
LOCUS       AX095547        21 bp    DNA             PAT       30-MAR-2001
DEFINITION  Sequence 725 from Patent WO0118250.
ACCESSION   AX095547
VERSION     AX095547.1  GI:13511750
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 725 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        4 a      1 c      11 g      4 t      1 others
ORIGIN


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  Best Local Similarity   86.7%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||||||||
Db     20 ACTCCACTCRCTCCA 6


RESULT   3
MUSAIC2A09/c
LOCUS       MUSAIC2A09     160 bp    DNA             ROD       27-APR-1993
DEFINITION  Mus musculus IL-3 receptor B-subunit (AIC2A) gene, exon 10.
ACCESSION   M94144
VERSION     M94144.1  GI:191815
KEYWORDS    IL-3 receptor B-subunit.
SEGMENT     9 of 13
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 160)
  AUTHORS   Gorman,D.M., Itoh,N., Jenkins,N.A., Gilbert,D.A., Copeland,N.G. and
            Miyajima,A.
  TITLE     Chromosomal localization and organization of the murine genes
            encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3,
            granulocyte/macrophage colony-stimulating factor, and interleukin 5
            receptors
  JOURNAL   J. Biol. Chem. 267, 15842-15848 (1992)
  MEDLINE   92348451
FEATURES             Location/Qualifiers
     source          1. .160
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
     exon            1. .160
                     /gene="AIC2A"
                     /number=10
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ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 7.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     132 GCTCCACTCGCTCCA 118


RESULT   4
MUSIL4R07/c
LOCUS       MUSIL4R07      207 bp    DNA             ROD       06-MAY-1996
DEFINITION  Mouse interleukin 4 receptor gene, exon 7.
ACCESSION   M64874
VERSION     M64874.1  GI:198354
KEYWORDS    interleukin 4 receptor.
SEGMENT     7 of 12
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE 1  (bases 1 to 207)
  AUTHORS   Wrighton,N., Campbell,L.A., Harada,N., Miyajima,A. and Lee,F.
  TITLE     The murine interleukin-4 receptor gene: genomic structure,
            expression and potential for alternative splicing
  JOURNAL   Growth Factors 6 (2), 103-118 (1992)
  MEDLINE   92265335
FEATURES              Location/Qualifiers
     source           1. .207
                      /organism="Mus musculus"
                      /strain="BALB/c"
                      /sub_species="domesticus"
                      /db_xref="taxon:10090"
                      /cell_type="sperm"
     intron           <1. .25
                      /note="putative"
                      /number=6
     exon             26. .182
                      /standard_name="'IL-4R'"
                      /note="'approx. 1.4kb 3' of segment 6'; 'interleukin-4
                      receptor'; putative"
                      /number=7
                      /label=exon7
     variation        31
                      /note="comparing genomic to cDNA; found in Balb/c"
                      /replace="a"
     intron           183. .>207
                      /note="putative"
                      /number=7
BASE COUNT       45 a     52 c     55 g     55 t
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     160 ACTCCACTCACTCCA 146


RESULT   5
D88111/c
LOCUS       D88111         213 bp    DNA             PRI       07-FEB-1999
DEFINITION  Homo sapiens DNA.
ACCESSION   D88111
VERSION     D88111.1  GI:1673297
KEYWORDS    .
SOURCE      Homo sapiens (strain:HeLa) DNA, clone_lib:libraly of clones
            containig poly(dG)poly(dC)library clone:pHGC40L.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 213)
  AUTHORS   Nishikawa,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-1996) to the DDBJ/EMBL/GenBank databases. Naoko
            Nishikawa, Univ. Tokyo, Ins. Mol. Cell. Biosci.; Yayoi 1-1-1,
            Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111(ex.7877),
            Fax:03-3818-9437)
REFERENCE   2  (bases 1 to 213)
  AUTHORS   Nishikawa,N., Oishi,M. and Kiyama,R.
  TITLE     Enrichment of poly(dG).poly(dC)-containing fragments from human
            genomic DNA by Mg2+-dependent triplex affinity capture
  JOURNAL   Unpublished (1996)
REFERENCE   3  (sites)
  AUTHORS   Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
  TITLE     Enrichment of oligo(dG).oligo(dC)-containing fragments from human
            genomic DNA by Mg 2+-dependent triplex affinity capture
  JOURNAL   Nucleic Acids Res. 25 (9), 1701-1708 (1997)
  MEDLINE   97263793
FEATURES              Location/Qualifiers
     source           1. .213
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ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     162 ACTCCATTCACTCCA 148


RESULT   6
ECIL7R1/c
LOCUS       ECIL7R1        248 bp    DNA             MAM       28-NOV-1999
DEFINITION  Equus caballus interleukin-7 receptor (IL7R) gene, partial
            sequence.
ACCESSION   AF115754
VERSION     AF115754.1  GI:6469582
KEYWORDS    .
SEGMENT     1 of 2
SOURCE      horse.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Caetano,A.R., Lyons,L.A., Laughlin,T.F., O'Brien,S.J., Murray,J.D.
            and Bowling,A.T.
  TITLE     Equine synteny mapping of comparative anchor tagged sequences
            (CATS) from human Chromosome 5
  JOURNAL   Mamm. Genome 10 (11), 1082-1084 (1999)
  MEDLINE   20028321
REFERENCE   2  (bases 1 to 248)
  AUTHORS   Caetano,A.R., Lyons,L.A., Laughlin,T.F., O'Brien,S.J., Murray,J.D.
            and Bowling,A.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-1998) Veterinary Genetics Lab., University of
            California Davis, One Shields Ave., Davis, CA 95616, USA
FEATURES              Location/Qualifiers
     source           1. .248
                      /organism="Equus caballus"
                      /db_xref="taxon:9796"
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ORIGIN
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  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     19 ACTCCATTCACTCCA 5


RESULT   7
G65440
LOCUS       G65440        367 bp    DNA             STS       19-JUL-2000
DEFINITION  stdJ388M5_151462 chromosome 22 genomic clone Homo sapiens STS
            genomic clone 388M5, sequence tagged site.
ACCESSION   G65440
VERSION     G65440.1  GI:9295650
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Dawson,E., Chen,Y., Hunt,S. and Dunham,I.
  TITLE     Extraction and analysis of SNP data from genomic sequence of human
            chromosome 22
  JOURNAL   Unpublished (1999)
COMMENT     Synonyms: stSG73865
            Contact: Ian Dunham
            Sanger Centre
            The Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, UK
            Email: idl@sanger.ac.uk
            Primer A: GAAGTGCAGAGGGAAACTGC
            Primer B: GACTCAGACCAGGTCCTGGA
            STS size: 367
            PCR Profile:
                  Presoak:         94 degrees C for  5.00 minutes
                  Denaturation:    93 degrees C for  30 seconds
                  Annealing:       60 degrees C for  30 seconds
                  Extension:       72 degrees C for  30 seconds
                  PCR Cycles:      35
                  Final Extension 72 degrees C for 5 minutes
                  Thermal Cycler: MJ Research (DNA Engine Tetrad)
            Protocol:
                  Template:        50-100 ng
                  Primer:          each 0.5 mM
                  dNTPs:           each 500 uM
                  BSA:             170ug/ml
                  2-mercaptoethanol: 10mM
                  Taq Polymerase: 0.04 units/ul
                  Total Vol:       15 ul

            Buffer:
                  6.7 mM MgCl2
                  67 mM Tris-HCl
                  16.7 mM (NH4)2SO4
                  pH:      8.8

            Accession of clone sequence : Z97055.
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                      /db_xref="taxon:9606"
                      /clone="388M5"
                      /clone_lib="chromosome 22 genomic clone"
     STS              1. .367
     primer_bind      1. .20
     primer_bind      complement(348. .367)
BASE COUNT       76 a    121 c     96 g     74 t
ORIGIN


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  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    337 ACTCCACTCACTCCA 351


RESULT   8
HSIL7R5/c
LOCUS       HSIL7R5       403 bp    DNA             PRI       05-DEC-1998
DEFINITION  Homo sapiens interleukin-7 receptor precursor (IL7R) gene, exon 5.
ACCESSION   AF043127
VERSION     AF043127.1  GI:3978158
KEYWORDS    .
SEGMENT     5 of 7
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 403)
  AUTHORS   Puel,A., Ziegler,S.F., Buckley,R.H. and Leonard,W.J.
  TITLE     Defective IL7R expression in T(-)B(+)NK(+) severe combined
            immunodeficiency
  JOURNAL   Nat. Genet. 20 (4), 394-397 (1998)
  MEDLINE   99057350
REFERENCE   2  (bases 1 to 403)
  AUTHORS   Puel,A., Ziegler,S.F., Buckley,R.H. and Leonard,W.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Immunology, Virginia Mason Research Center,
            1000 Seneca St., Seattle, WA 98101, USA
FEATURES              Location/Qualifiers
     source           1. .403
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
     exon             140. .308
                      /gene="IL7R"
                      /number=5
BASE COUNT      126 a     81 c     87 g    109 t
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 8.2e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    265 ACTCCATTCACTCCA 251


RESULT   9
I21102/c
LOCUS       I21102        490 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 73 from patent US 5518880.
ACCESSION   I21102
VERSION     I21102.1  GI:1601456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Leonard,W.J., Noguchi,M. and McBride,O.Wesley.
  TITLE     Methods for diagnosis of XSCID and kits thereof
  JOURNAL   Patent: US 5518880-A 73 21-MAY-1996;
FEATURES              Location/Qualifiers
     source           1. .490
                      /organism="unknown"
BASE COUNT      122 a    127 c    110 g    130 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 10;  Length 490;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
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  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
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Db    254 GCTCCATTCACTCCA 240


RESULT  10
HUMIL2RG05/c
LOCUS       HUMIL2RG05    490 bp    DNA             PRI       06-JAN-1995
DEFINITION  Human interleukin 2 receptor gamma chain (IL2RG) gene, exon 5.
ACCESSION   L12180
VERSION     L12180.1  GI:307053
KEYWORDS    interleukin 2 receptor gamma chain.
SEGMENT     5 of 8
SOURCE      Homo sapiens (tissue library: Charon 4A) fetus liver DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Noguchi,M., Adelstein,S., Cao,X. and Leonard,W.J.
  TITLE     Characterization of the human interleukin-2 receptor gamma chain
            gene
  JOURNAL   J. Biol. Chem. 268 (18), 13601-13608 (1993)
  MEDLINE   93293887
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /dev_stage="fetus"
                     /tissue_type="liver"
                     /tissue_lib="Charon 4A"
                     /map="Xq13"
     intron          order(L12179.1:221. .423,1. .125)
                     /gene="IL2RG"
                     /number=4
     exon            126. .288
                     /gene="IL2RG"
                     /number=5
BASE COUNT      122 a    127 c    110 g    130 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 97;  Length 490;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    254 GCTCCATTCACTCCA 240


RESULT  11
CNS01DQR/c
LOCUS       CNS01DQR      537 bp    mRNA            PLN       03-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL117163
VERSION     AL117163.1  GI:5832379
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 537)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .537
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W01G091"
BASE COUNT      137 a     46 c    178 g    176 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 14;  Length 537;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    265 ACTCCACTCACTCCA 251


RESULT  12
AC072998/c
LOCUS       AC072998      572 bp    DNA             HTG       07-JUN-2000
DEFINITION  Giardia intestinalis clone NJ4660 strain WB-C6, LOW-PASS SEQUENCE
            SAMPLING.
ACCESSION   AC072998
VERSION     AC072998.1  GI:8325346
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Giardia intestinalis.
  ORGANISM  Giardia intestinalis
            Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U.,
            Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
  TITLE     Giardia: a model for ancient eukaryotic genome analysis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 572)
  AUTHORS   Nixon,J., Morrison,H.G., McArthur,A.G., Eakin,N.Q., Kim,U.,
            Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-2000) Josephine Bay Paul Center for Comparative
            Molecular Biology and Evolution, Marine Biological Laboratory, 7
            MBL Street, Woods Hole, MA 02543-1015, USA
COMMENT     * NOTE: This record contains 1 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *         1      572: contig of 572 bp in length.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Giardia intestinalis"
                     /strain="WB-C6"
                     /db_xref="taxon:5741"
                     /clone="NJ4660"
BASE COUNT      150 a    133 c    151 g    134 t      4 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 74;  Length 572;
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```
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    311 GCTCCACTCACTCCA 297

RESULT 13
AC030504/c
LOCUS       AC030504      585 bp    DNA             HTG       02-APR-2000
DEFINITION  Giardia intestinalis clone EI0461 strain WB-C6, LOW-PASS SEQUENCE
            SAMPLING.
ACCESSION   AC030504
VERSION     AC030504.1  GI:7385833
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Giardia intestinalis.
  ORGANISM  Giardia intestinalis
            Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U.,
            Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
  TITLE     Giardia: a model for ancient eukaryotic genome analysis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 585)
  AUTHORS   Eakin,N.Q., Morrison,H.G., McArthur,A.G., Nixon,J., Kim,U.,
            Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2000) Josephine Bay Paul Center for Comparative
            Molecular Biology and Evolution, Marine Biological Laboratory, 7
            MBL Street, Woods Hole, MA 02543-1015, USA
COMMENT     * NOTE: This record contains 1 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *       1      585: contig of 585 bp in length.
FEATURES            Location/Qualifiers
     source         1. .585
                    /organism="Giardia intestinalis"
                    /strain="WB-C6"
                    /db_xref="taxon:5741"
                    /clone="EI0461"
BASE COUNT      144 a    140 c    150 g    145 t      6 others
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 71;  Length 585;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     76 GCTCCACTCACTCCA 62

RESULT 14
AF029294/c
LOCUS       AF029294      652 bp    mRNA            MAM       22-JUL-1999
DEFINITION  Mustela vison prolactin receptor (PRLr) mRNA, partial cds.
ACCESSION   AF029294
VERSION     AF029294.1  GI:2688974
KEYWORDS    .
SOURCE      American mink.
  ORGANISM  Mustela vison
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   Douglas,D.A., Houde,A., Song,J.H., Farookhi,R., Concannon,P.W. and
            Murphy,B.D.
  TITLE     Luteotropic hormone receptors in the ovary of the mink (Mustela
            vison) during delayed implantation and early-postimplantation
            gestation
  JOURNAL   Biol. Reprod. 59 (3), 571-578 (1998)
  MEDLINE   98384190
   PUBMED   9716555
REFERENCE   2  (bases 1 to 652)
  AUTHORS   Douglas,D.A., Song,J.-H., Houde,A. and Murphy,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-1997) Agriculture and Agri-Food Canada, Food
            Research and Development Centre, 3600 Casavant Blvd. West,
            St-Hyacinthe, Quebec J2S 8E3, Canada
FEATURES            Location/Qualifiers
     source         1. .652
                    /organism="Mustela vison"
                    /db_xref="taxon:9667"
                    /tissue_type="testis"
     gene           <1. .>652
                    /gene="PRLr"
     CDS            <1. .>652
                    /gene="PRLr"
                    /codon_start=2
                    /product="prolactin receptor"
                    /protein_id="AAB88899.1"
                    /db_xref="GI:2688975"
                    /translation="KPGEDGGLPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKH
                    TSIWTMYIITINATNEMGSSSSDPRYVTLTYIVEPDPPVNLSLELKQPEDKKTYLWIK
                    WYPPTLVDVRSGWLTLQYEIRLKPEKATEWETHFAGLQTQFKILSLYPGQKYLVQVRC
                    KPDHGFWSEWSPKRSIQIPNDISMKDTIVWIFVAVLSAVICLIMVAAVALKGHSMVT"
BASE COUNT      195 a    159 c    145 g    153 t
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 7;  Length 652;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    514 GCTCCACTCACTCCA 500

RESULT 15
AF169792/c
LOCUS       AF169792      681 bp    mRNA            MAM       07-SEP-2000
DEFINITION  Ursus maritimus prolactin receptor mRNA, partial cds.
ACCESSION   AF169792
VERSION     AF169792.1  GI:9988483
KEYWORDS    .
SOURCE      polar bear.
  ORGANISM  Ursus maritimus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Howell-Skalla,L.A., Bunick,D., Bleck,G.T., Nelson,R.A. and
            Bahr,J.M.
  TITLE     Cloning, sequence analysis, and seasonal mRNA expression of the
            extracellular region of the luteinizing hormone receptor (LHr),
            follicle-stimulating hormone receptor (FSHr), and prolactin
            receptor (PRLr) genes in the testis of the black bear (Ursus
            americanus)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 681)
  AUTHORS   Howell-Skalla,L.A. and Bahr,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-1999) Curriculum in Toxicology, University of
            North Carolina, MD-72, US EPA, Research Triangle Park, NC 27711,
            USA
FEATURES            Location/Qualifiers
     source         1. .681
```

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                     /organism="Ursus maritimus"
                     /db_xref="taxon:29073"
                     /tissue_type="liver"
     primer_bind     1. .22
     CDS             <1. .>681
                     /note="PRLr"
                     /codon_start=1
                     /product="prolactin receptor"
                     /protein_id="AAG10648.1"
                     /db_xref="GI:9988484"
                     /translation="KETFTCWWKPGEDGGLPTNYTLTYRKEGETTTHECPDYISSGPN
                     SCYFNKKHTSIWTMYIITINATNQMGSSSSDPRYVDVTYIVEPDPPVNLTLELKQPED
                     KKPYLWMKWYPPTLVDVRSGWLTLQYEIRLKPEKATEWETHFAGQQTQFKILSLYPGQ
                     KYLVQVRCKPDHGFWSEWSPESSIQIPNDVTMKDTIVWIFVAVLSAVICLIMVAAVAL
                     KGHSMVTCI"
     primer_bind     complement(662. .681)
BASE COUNT      200 a    163 c    158 g    160 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 7;  Length 681;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :||||||:||:|||||
Db     537 GCTCCACTCACTCCA 523


Search completed: August 29, 2001, 19:51:55
Job time: 17233 sec
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```
RESULT  15
AW165758
LOCUS       AW165758      315 bp    mRNA            EST       12-NOV-1999
DEFINITION  MBAsBWA080M13R Ascaris suum (parasitic nematode) body wall muscle
            and hypodermis Ascaris suum cDNA clone MBAsBWA080 5', mRNA
            sequence.
ACCESSION   AW165758
VERSION     AW165758.1  GI:6382633
KEYWORDS    EST.
SOURCE      pig roundworm.
  ORGANISM  Ascaris suum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea
            ; Ascarididae; Ascaris.
REFERENCE   1  (bases 1 to 315)
  AUTHORS   Daub,J., Geary,T. and Blaxter,M.
  TITLE     A survey of genes expressed in the parasitic nematode Ascaris suum
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The Ascaris suum EST dataset (including the ASC clustering
            information) is available on the www at http://www.ed.ac.uk/(tilde
            )mbx/AscarisWeb/AscarisEST.html
            PCR PRimers
            FORWARD: M13 Reverse (AGCGGATAACAATTTCACACAGGA)
            BACKWARD: M13 Forward (CGCCAGGGTTTTCCCAGTCACGAC)
            Seq primer: M13 Reverse (AGCGGATAACAATTTCACACAGGA).
FEATURES             Location/Qualifiers
     source          1. .315
                     /organism="Ascaris suum"
                     /db_xref="taxon:6253"
                     /clone="MBAsBWA080"
                     /clone_lib="Ascaris suum (parasitic nematode) body wall
                     muscle and hypodermis"
                     /sex="mixed"
                     /tissue_type="body wall muscle and hypodermis"
                     /dev_stage="adult"
                     /note="Vector: Lambda Zap II; Site_1: NotI (5'end);
                     Site_2: NotI (3'end); Ascaris suum is an intestinal
                     nematode parasite of pigs. The library was constructed
                     from dissected body wall muscle and hypodermis tissue for
                     Dr. T. Geary, Pharmacia-Upjohn Inc, Kalamazoo, MI, USA
                     [tggeary@am.pnu.com]"
BASE COUNT       34 a    105 c     98 g     78 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 112;  Length 315;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     132 GCTCCATTCGCTCCA 146


Search completed: August 29, 2001, 19:22:10
Job time: 24133 sec
```

```
                FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT       60 a     77 c     60 g    102 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 123;  Length 299;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db      1 ACTCCATTCACTCCA 15


RESULT  13
AV298115
LOCUS       AV298115      302 bp    mRNA            EST       10-NOV-1999
DEFINITION  AV298115 RIKEN full-length enriched, 8 days embryo Mus musculus
            cDNA clone 5730454J22 3', mRNA sequence.
ACCESSION   AV298115
VERSION     AV298115.1  GI:6330360
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
            ,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
            Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,
            Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
            Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
            ,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5730454J22"
                     /clone_lib="RIKEN full-length enriched, 8 days embryo"
                     /sex="mixed"
                     /dev_stage="8 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of subtraction to
                     Rot = 100.0 Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT       76 a     92 c     70 g     64 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 28;  Length 302;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     86 GCTCCACTCACTCCA 100


RESULT  14
AQ937634
LOCUS       AQ937634      313 bp    DNA             GSS       23-AUG-2000
DEFINITION  NB6-223C Human NotI clones Homo sapiens genomic, DNA sequence.
ACCESSION   AQ937634
VERSION     AQ937634.1  GI:7214012
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 313)
  AUTHORS   Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie
            ,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J.,
            Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
  TITLE     NotI clones in the analysis of the human genome
  JOURNAL   Nucleic Acids Res. 28 (7), 1635-1639 (2000)
  MEDLINE   20175728
COMMENT     Contact: Podowski RM
            Center for Genomics Research
            Karolinska Institute
            17177 Stockholm, Sweden
            Tel: +46-8-728-6372
            Fax: +46-8-337983
            Email: Raf.Podowski@cgr.ki.se
            Class: NotI site.
FEATURES             Location/Qualifiers
     source          1. .313
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human NotI clones"
BASE COUNT       47 a    148 c     74 g     43 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 235;  Length 313;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    191 ACTCCACTCACTCCA 205
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .297
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5930436B16"
/clone_lib="RIKEN full-length enriched, 13 days embryo forelimb"
/sex="mixed"
/tissue_type="forelimb"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT 93 a 60 c 45 g 99 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 124; Length 297;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTCRCTCCA 15
:|||||:||:|||||
Db 20 ACTCCATTCACTCCA 34

RESULT 12
BB024897
LOCUS BB024897 299 bp mRNA EST 23-JUN-2000
DEFINITION BB024897 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330424O07 3', mRNA sequence.
ACCESSION BB024897
VERSION BB024897.1 GI:8198974
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 299)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M. , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y. , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y. , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I. , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino ,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .299
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5330424O07"
/clone_lib="RIKEN full-length enriched, adult male pituitary gland"
/sex="male"
/tissue_type="pituitary gland"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda

```
           ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
           , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
           ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE    RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL  Unpublished (2000)
COMMENT    Contact: Yoshihide Hayashizaki
           Genome Exploration Research Group, Life Science Tsukuba Center,
           Genome Science Laboratory
           The Institute of Physical and Chemical Research (RIKEN), Genomic
           Sciences Center
           3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
           Tel: +81-298-36-9013
           Fax: +81-298-36-9098
           Email: genome-res@rtc.riken.go.jp,
           URL:http://genome.rtc.riken.go.jp/
           Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
           ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
           Thermostabilization and thermoactivation of thermolabile enzymes by
           trehalose and its application for the synthesis of full length
           cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
            Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
           Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
           ,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
           system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .295
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5330420L02"
                     /clone_lib="RIKEN full-length enriched, adult male
                     pituitary gland"
                     /sex="male"
                     /tissue_type="pituitary gland"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 3.0 and subtraction to Rot = 100.0. Second strand
                     cDNA was prepared with the primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT       90 a     77 c     57 g     71 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 123;  Length 295;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     184 ACTCCATTCACTCCA 170


RESULT  10
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AF061117/c
LOCUS       AF061117      297 bp    mRNA            EST       06-MAY-1998
DEFINITION  AF061117 Rice Millyang 117 suspension culture mRNA Oryza sativa
            cDNA clone F25109, mRNA sequence.
ACCESSION   AF061117
VERSION     AF061117.1  GI:3114679
KEYWORDS    EST.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 297)
  AUTHORS   Kim,C.Y., Cheon,S.Y. and Cho,M.J.
  TITLE     Isolation and Characterization of Fungal Elicitor Responsive Rice
            Genes by mRNA Differential Display
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Kim, Cha Young
            Biochemistry
            PMBBRC
            900 Gajwa-dong, Chinju, Kyeong-nam 660-701, Korea
            Email: choslab@nongae.gsnu.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .297
                     /organism="Oryza sativa"
                     /cultivar="Millyang 117"
                     /db_xref="taxon:4530"
                     /clone="F25109"
                     /clone_lib="Rice Millyang 117 suspension culture mRNA"
                     /note="suspension culture"
BASE COUNT       77 a     66 c     70 g     84 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 14;  Length 297;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      78 ACTCCATTCACTCCA 64


RESULT  11
BB038288
LOCUS       BB038288      297 bp    mRNA            EST       23-JUN-2000
DEFINITION  BB038288 RIKEN full-length enriched, 13 days embryo forelimb Mus
            musculus cDNA clone 5930436B16 3' similar to U01135 Mus musculus
            B6D2F1 clone 2A-1 mRNA, mRNA sequence.
ACCESSION   BB038288
VERSION     BB038288.1  GI:8444674
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 297)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
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  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      16 ACTCCATTCACTCCA 30


RESULT   7
AW417497/c
LOCUS       AW417497      275 bp    mRNA            EST       09-JUL-2000
DEFINITION  54258 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW417497
VERSION     AW417497.1  GI:6945379
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 20  row: K  column: 3
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .275
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT       65 a     59 c     83 g     66 t      2 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 115;  Length 275;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      64 GCTCCATTCACTCCA 50


RESULT   8
AA562009/c
LOCUS       AA562009      287 bp    mRNA            EST       18-AUG-1997
DEFINITION  vl21g04.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
            IMAGE:972918 5' similar to gb:M29697 Mouse interleukin-7 receptor
            (MOUSE);, mRNA sequence.
ACCESSION   AA562009
VERSION     AA562009.1  GI:2333474
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 287)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:553646
            Putative full length read
            vector to vector length is 288
            Seq primer: -28m13 rev1 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .287
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:972918"
                     /clone_lib="Stratagene mouse Tcell 937311"
                     /tissue_type="Tcell"
                     /dev_stage="M30 CD4+ cells"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       84 a     70 c     59 g     74 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 9;  Length 287;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     160 ACTCCACTCGCTCCA 146


RESULT   9
BB024272/c
LOCUS       BB024272      295 bp    mRNA            EST       23-JUN-2000
DEFINITION  BB024272 RIKEN full-length enriched, adult male pituitary gland Mus
            musculus cDNA clone 5330420L02 3', mRNA sequence.
ACCESSION   BB024272
VERSION     BB024272.1  GI:8197502
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 295)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
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  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    107 ACTCCACTCGCTCCA 121


RESULT   5
AQ548570/c
LOCUS       AQ548570      256 bp    DNA             GSS       28-MAY-1999
DEFINITION  CITBI-E1-2635F16.TF CITBI-E1 Homo sapiens genomic clone 2635F16,
            DNA sequence.
ACCESSION   AQ548570
VERSION     AQ548570.1  GI:4903833
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2635F16"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT       65 a     50 c     99 g     42 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 230;  Length 256;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    175 GCTCCACTCACTCCA 161


RESULT   6
BB051888
LOCUS       BB051888      258 bp    mRNA            EST       25-JUN-2000
DEFINITION  BB051888 RIKEN full-length enriched, 12 days embryo male wolffian
            duct Mus musculus cDNA clone 6720436D12 3' similar to U01135 Mus
            musculus B6D2F1 clone 2A-1 mRNA, mRNA sequence.
ACCESSION   BB051888
VERSION     BB051888.1  GI:8459036
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .258
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="6720436D12"
                     /clone_lib="RIKEN full-length enriched, 12 days embryo
                     male wolffian duct"
                     /sex="male"
                     /tissue_type="wolffian duct includes surrounding region"
                     /dev_stage="12 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
BASE COUNT       85 a     48 c     44 g     81 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 124;  Length 258;
```

```
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 40  row: J  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .173
                      /organism="Bos taurus"
                      /db_xref="taxon:9913"
                      /clone_lib="MARC 3BOV"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                      Library made from pooled tissue from marrow, alveolar
                      macrophage, ovary, fetal semitendonosus muscle, and fetal
                      longissimus muscle."
BASE COUNT       26 a     38 c     59 g     50 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 151;  Length 173;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     23 GCTCCATTCACTCCA 9


RESULT   3
BE076128/c
LOCUS       BE076128      201 bp    mRNA          EST       09-JUN-2000
DEFINITION  MR2-BT0590-100300-118-c08_1 BT0590 Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BE076128
VERSION     BE076128.1  GI:8425639
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 201)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR2-BT0590-100
            300-118-c08_1&t3=2000-03-10&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 201.
FEATURES              Location/Qualifiers
     source           1. .201
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="BT0590"
                      /dev_stage="Adult"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No. 196
                      ,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
BASE COUNT       30 a     50 c     71 g     50 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 163;  Length 201;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     43 GCTCCACTCACTCCA 29


RESULT   4
AI505954
LOCUS       AI505954      248 bp    mRNA          EST       11-MAR-1999
DEFINITION  v121f12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
            IMAGE:972911 3' similar to gb:M29697 Mouse interleukin-7 receptor
            (MOUSE);, mRNA sequence.
ACCESSION   AI505954
VERSION     AI505954.1  GI:4403805
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:553639
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end.
FEATURES              Location/Qualifiers
     source           1. .248
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:972911"
                      /clone_lib="Stratagene mouse Tcell 937311"
                      /tissue_type="Tcell"
                      /dev_stage="M30 CD4+ cells"
                      /lab_host="SOLR (kanamycin resistant)"
                      /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                      Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
                      Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                      3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       63 a     49 c     60 g     76 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 248;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.8	92.0	151	149	BF458328	BF458328 UI-M-BZ1-
c 2	13.8	92.0	173	151	BF601415	BF601415 266391 MA
c 3	13.8	92.0	201	163	BE076128	BE076128 MR2-BT059
4	13.8	92.0	248	21	AI505954	AI505954 vl21f12.x
c 5	13.8	92.0	256	230	AQ548570	AQ548570 CITBI-E1-
6	13.8	92.0	258	124	BB051888	BB051888 BB051888
c 7	13.8	92.0	275	115	AW417497	AW417497 54258 MAR
c 8	13.8	92.0	287	9	AA562009	AA562009 vl21g04.r
c 9	13.8	92.0	295	123	BB024272	BB024272 BB024272
c 10	13.8	92.0	297	14	AF061117	AF061117 AF061117
11	13.8	92.0	297	124	BB038288	BB038288 BB038288
12	13.8	92.0	299	123	BB024897	BB024897 BB024897
13	13.8	92.0	302	28	AV298115	AV298115 AV298115
14	13.8	92.0	313	235	AQ937634	AQ937634 NB6-223C
15	13.8	92.0	315	112	AW165758	AW165758 MBAsBWA08
16	13.8	92.0	331	111	AW057700	AW057700 wx02c04.x
17	13.8	92.0	335	190	W23972	W23972 zb47a01.r1
18	13.8	92.0	338	148	BF425404	BF425404 su43c09.y
c 19	13.8	92.0	341	2	AA083143	AA083143 zn08b04.r
c 20	13.8	92.0	341	13	AA921043	AA921043 vy75h06.r
c 21	13.8	92.0	343	138	BE685591	BE685591 187957 MA
c 22	13.8	92.0	349	115	AW417922	AW417922 55277 MAR
c 23	13.8	92.0	353	30	AV406268	AV406268 AV406268
c 24	13.8	92.0	356	136	BE517357	BE517357 WHE0625_D
25	13.8	92.0	360	9	AA621766	AA621766 af06d10.s
26	13.8	92.0	365	230	AQ545960	AQ545960 CITBI-E1-
c 27	13.8	92.0	366	150	BF524586	BF524586 UI-R-AD0-
28	13.8	92.0	376	111	AW074425	AW074425 xa93a07.x
c 29	13.8	92.0	376	222	FR0029534	AL025903 Fugu rubr
c 30	13.8	92.0	389	115	AW406187	AW406187 UI-HF-BL0
c 31	13.8	92.0	396	154	BG516644	BG516644 EtESTed59
32	13.8	92.0	407	231	AQ669609	AQ669609 HS_5364_A
33	13.8	92.0	413	22	AI633127	AI633127 tz19d11.x
c 34	13.8	92.0	413	154	BG516645	BG516645 EtESTed59
c 35	13.8	92.0	419	151	BF599654	BF599654 263517 MA
c 36	13.8	92.0	422	170	BF880060	BF880060 IL3-ET011
37	13.8	92.0	427	110	AW005961	AW005961 wz80g07.x
c 38	13.8	92.0	430	170	BF880064	BF880064 IL3-ET011
c 39	13.8	92.0	436	150	BF559553	BF559553 UI-R-A1-d
c 40	13.8	92.0	438	142	BE926519	BE926519 MR4-BT039
c 41	13.8	92.0	441	234	AQ813137	AQ813137 HS_5300_A
42	13.8	92.0	443	13	AA909507	AA909507 ol16d11.s
43	13.8	92.0	446	110	AW001800	AW001800 ws05c01.x
44	13.8	92.0	458	1	AA043001	AA043001 zk56f01.r
45	13.8	92.0	459	22	AI559567	AI559567 tq50f02.x

ALIGNMENTS

```
RESULT   1
BF458328/c
LOCUS       BF458328      151 bp    mRNA            EST       01-DEC-2000
DEFINITION  UI-M-BZ1-blp-e-08-0-UI.s1 NIH_BMAP_MHI2_S1 Mus musculus cDNA clone
            UI-M-BZ1-blp-e-08-0-UI 3', mRNA sequence.
ACCESSION   BF458328
VERSION     BF458328.1  GI:11524497
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 151)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .151
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BZ1-blp-e-08-0-UI"
                     /clone_lib="NIH_BMAP_MHI2_S1"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_MHI2_S1 library is a subtracted library derived
                     from  NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived
                     from mouse hippocampus tissue. For a detailed description
                     of the library from which this clone was derived, please
                     visit our web site at brainest.eng.uiowa.edu.
                     TAG_SEQ=None found"
BASE COUNT       31 a      34 c      48 g      38 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 149;  Length 151;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     101 ACTCCACTCGCTCCA 87


RESULT   2
BF601415/c
LOCUS       BF601415      173 bp    mRNA            EST       13-DEC-2000
DEFINITION  266391 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BF601415
VERSION     BF601415.1  GI:11698637
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 173)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
            ,W.W. and Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
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254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 12:39:57 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-6
Perfect score: 15
Sequence: 1 RCTCCAYTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: gb_est2:*
3: gb_est3:*
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54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estom1:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

PT for diagnosis or detection
XX
PS Claim 10; Page 46; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 465 BP; 158 A; 79 C; 92 G; 135 T; 1 other;

Query Match 92.0%; Score 13.8; DB 19; Length 465;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db    185 ACTCCACTCACTCCA 171
```

Search completed: August 29, 2001, 20:16:40
Job time: 7421 sec

```
XX
CC   This sequence represents a PCR amplified fragment of the mouse
CC   haemopoietin receptor protein family NR8 gene. The sequence was used to
CC   isolate further mouse NR8 genes. Antibodies to the NR8 family proteins
CC   are used for the diagnosis of blood formation disorders. Compounds
CC   identified as binding to the proteins are used for the treatment of
CC   such disorders.
XX
SQ   Sequence 330 BP; 72 A; 96 C; 94 G; 68 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 330;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     297 ACTCCATTCACTCCA 283


RESULT  14
AAA89731/c
ID   AAA89731 standard; cDNA; 444 BP.
XX
AC   AAA89731;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Mouse IL-3 receptor nucleotide sequence #2.
XX
KW   Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
KW   antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant;
KW   vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW   digestion disorder; wound healing disorder; gene therapy; ss.
XX
OS   Mus sp.
XX
PN   WO200043419-A2.
XX
PD   27-JUL-2000.
XX
PF   20-JAN-2000; 2000WO-US01431.
XX
PR   20-JAN-1999;   99US-0116534.
PR   26-JAN-1999;   99US-0117274.
PR   26-JAN-1999;   99US-0117308.
PR   26-JAN-1999;   99US-0117309.
PR   26-JAN-1999;   99US-0117312.
PR   01-FEB-1999;   99US-0118177.
PR   01-FEB-1999;   99US-0118178.
PR   01-FEB-1999;   99US-0118179.
PR   09-FEB-1999;   99US-0119286.
PR   11-FEB-1999;   99US-0119998.
PR   11-FEB-1999;   99US-0119759.
XX
PA   (RIGE-) RIGEL PHARM INC.
XX
PI   Luo Y;
XX
DR   WPI; 2000-482908/42.
XX
PT   New nucleic acids encoding Exo proteins which are useful in the
PT   diagnosis, treatment or prevention of exocytosis-mediated disorders
PT   such as asthma, inflammation and allergies -
XX
PS   Disclosure; Page 301-302; 305pp; English.
XX
CC   The present sequence encodes a polypeptide which is associated with
CC   the exocytosis pathway. cDNA molecules encoding proteins involved in
CC   exocytosis have been isolated by yeast one-hybrid and two-hybrid
CC   screening. Novel proteins, termed Exo proteins, have been identified that
CC   interact with known exocytosis-associated proteins such as GS27, alpha
CC   snap, unc18-1, vamp3, snap-23, and the rab family of proteins.
CC   Exo proteins and their agonists and antagonists are useful in the
CC   diagnosis, treatment or prevention of exocytosis-mediated disorders
CC   such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
CC   (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC   diabetes, digestion disorders and wound healing disorders.
CC   The nucleic acids, antagonists or agonists of Exo proteins are useful
CC   in gene therapy. The nucleic acids are also useful for generating
CC   transgenic or knock-out animals which can be used in the
CC   development and screening of therapeutically useful reagents.
XX
SQ   Sequence 444 BP; 124 A; 115 C; 115 G; 87 T; 3 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 444;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db     249 GCTCCACTCGCTCCA 235


RESULT  15
AAV22698/c
ID   AAV22698 standard; DNA; 465 BP.
XX
AC   AAV22698;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Interleukin-13 binding protein C-terminal region gene.
XX
KW   Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW   autoimmune disease; antibody; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..465
FT                   /*tag= a
FT                   /product= "IL-13 binding protein Open Reading Frame 1"
FT                   /note= "No start codon, stop codons given within
FT                         sequence."
FT   CDS             2..463
FT                   /*tag= b
FT                   /product= "IL-13 binding protein ORF 2"
FT                   /note= "No start codon, stop codons given within
FT                         sequence."
FT   CDS             3..455
FT                   /*tag= c
FT                   /product= "IL-13 binding protein ORF 3"
FT                   /note= "No start codon, stop codons given within
FT                         sequence."
XX
PN   WO9810638-A1.
XX
PD   19-MAR-1998.
XX
PF   10-SEP-1997;   97WO-AU00591.
XX
PR   27-FEB-1997;   97AU-0005374.
PR   10-SEP-1996;   96AU-0002262.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Hilton DJ,  Nicola NA,  Simpson RJ,  Zhang J;
XX
DR   WPI; 1998-207062/18.
DR   P-PSDB; AAW56255, AAW56256, AAW56257.
XX
PT   New isolated interleukin-13 binding protein - used to develop
PT   products for therapy e.g. for allergic conditions such as asthma or
```

XX
PR 13-MAR-1996; 96US-0013345.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX
DR WPI; 1997-470820/43.
XX
PT New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX
PS Example 1; Page 59; 79pp; English.
XX
CC AAT96787 and AAT96788 are primers designed from the sequences of two
CC expressed sequence tags (EST's) and are used in a 3' RACE (rapid
CC amplification of cDNA ends) reaction to amplify the novel ligand-binding
CC receptor, Zcytor2, from humans and macaques. Zcytor2 is a receptor for
CC cytokines (particularly interleukin-13) expressed on the surface of
CC testicular cells, probably being involved in spermatogenesis. It can be
CC used to detect ligands that promote proliferation and/or differentiation
CC of such cells in cultures and may also be used to treat infertility.
CC Antagonists of this receptor may be used to characterise ligand-receptor
CC interactions and as male-specific contraceptives. By blocking the action
CC of IL-13, receptor antagonists and ligand-binding this receptor can also
CC be used to modulate immune function, e.g. in allergy and asthma, as a
CC diagnostic to determine circulating levels of ligand and also to isolate
CC and purify ligands. Antibodies can be used to assay circulating receptor
CC (an abnormal level may be indicative of disease such as cancer), for
CC labelling cells that express the receptor, and therapeutically as
CC antagonist.
XX
SQ Sequence 25 BP; 6 A; 1 C; 11 G; 7 T; 0 other;

Query Match 92.0%; Score 13.8; DB 18; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTCRCTCCA 15
:|||||:||:|||||
Db 22 ACTCCACTCACTCCA 8

RESULT 12
AAA61554/c
ID AAA61554 standard; DNA; 71 BP.
XX
AC AAA61554;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human IL-5R alpha chain-IgG4 hinge/CH2 domain PCR primer, SEQ ID NO:15.
XX
KW Human; secreted Klotho/Ig heavy chain constant region chimeric protein;
KW immunoglobulin G4; gene therapy; antibody; antiarthritic; nephrotropic;
KW kidney disease; oedema; dropsy; arthritis; IgG1 heavy chain; hinge;
KW CH2 domain; IL-5R alpha chain; interleukin-5 receptor; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200027885-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-JP06152.
XX
PR 05-NOV-1998; 98JP-0314153.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Kato Y, Nabeshima Y;
XX
DR WPI; 2000-376499/32.
XX
PT Chimeric polypeptide containing klotho protein bound to an
PT immunoglobulin for treatment and prevention of kidney disease, dropsy
PT and arthritis -
XX
PS Example 1; Page 89; 94pp; Japanese.
XX
CC The invention relates to chimeric proteins comprising the human Klotho
CC protein fused to a human immunoglobulin (AAB11691-B11694), and to DNA
CC sequences encoding them (AAA61542-A61545). It also relates to gene
CC therapy vectors comprising DNA encoding the chimeric proteins of the
CC invention, to detection and assay of molecules which interact with
CC Klotho, to antibodies raised against the chimeric protein and to a
CC diagnostic method for Klotho-related disorders using the antibodies. The
CC chimeric proteins of the invention have antiarthritic and nephrotropic
CC activity, and may be used for the treatment, prevention and diagnosis of
CC disorders with which Klotho is associated, including kidney disease,
CC oedema (dropsy) and arthritis. Sequences AAA61554-A61557 represent PCR
CC primers used in an exemplification of the invention to generate and
CC amplify DNA encoding the human IL-5 receptor (interleukin-5 receptor)
CC alpha chain and the hinge and part of the CH2 domain of the human IgG4
CC (immunoglobulin G4) heavy chain.
XX
SQ Sequence 71 BP; 16 A; 13 C; 25 G; 17 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 71;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTCRCTCCA 15
:|||||:||:|||||
Db 55 GCTCCACTCACTCCA 41

RESULT 13
AAZ59255/c
ID AAZ59255 standard; DNA; 330 BP.
XX
AC AAZ59255;
XX
DT 24-MAY-2000 (first entry)
XX
DE Fragment of mouse NR8 sequence used as a probe.
XX
KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; ds.
XX
OS Mus sp.
XX
PN WO9967290-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-JP03351.
XX
PR 24-JUN-1998; 98JP-0214720.
PR 19-OCT-1998; 98JP-0297409.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
DR WPI; 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders -
XX
PS Example 7; Page 172-173; 176pp; Japanese.

```
KW   cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW   PCR; primer; amplification; Human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9811225-A2.
XX
PD   19-MAR-1998.
XX
PF   11-SEP-1997;   97WO-GB02479.
XX
PR   11-SEP-1996;   96AU-0002246.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PA   (DZIE/) DZIEGLEWSKA H E.
XX
PI   Alexander W,  Fabri L,  Farley A,  Hilton DJ,  Kikuchi Y;
PI   Kojima T,  Maeda M,  Nash A,  Nicola NA,  Rakar S,  Willson T;
PI   Zhang J;
XX
DR   WPI; 1998-260970/23.
XX
PT   New isolated haemopoietin receptor - used for developing products
PT   for modulating proliferation, differentiation and survival of cells,
PT   e.g. neuronal cells
XX
PS   Example 16; Page 66; 182pp; English.
XX
CC   The probe AAV27166 and primers AAV27167-V27168 were used in a method of
CC   the invention to isolate NR6 a novel haemopoietin receptor (HR).
CC   Interaction between the novel HR and a ligand facilitates proliferation,
CC   differentiation and survival of a wide variety of cells.  The HR and
CC   it's derivatives can be used for modulating the activity of the receptors
CC   e.g. to regulate development, maintenance or regeneration in an array of
CC   different cells and tissues in vitro and in vivo.  They can be present
CC   in therapeutics used for modulating neuronal proliferation,
CC   differentiation and survival.  The products can also be used for
CC   detection and diagnosis, e.g. for cancers or predisposition to cancers,
CC   or for drug screening.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 4 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 19;  Length 18;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db       2 gctccactcgctcca 16


RESULT  10
AAF95960/c
ID   AAF95960 standard; DNA; 21 BP.
XX
AC   AAF95960;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #721.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US24503.
XX
PR   10-SEP-1999;   99US-0153357.
PR   26-JUL-2000; 2000US-0220947.
PR   16-AUG-2000; 2000US-0225724.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  McCarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis -
XX
PS   Examples; Page 98; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism
CC   and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification.
XX
SQ   Sequence 21 BP; 4 A; 2 C; 11 G; 4 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 22;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      20 ACTCCACTCGCTCCA 6


RESULT  11
AAT96787/c
ID   AAT96787 standard; cDNA; 25 BP.
XX
AC   AAT96787;
XX
DT   30-MAR-1998  (first entry)
XX
DE   Human and macaque Zcytor2 cytokine receptor primer ZG9803.
XX
KW   Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW   infertility; antagonist; contraceptive; diagnostic; therapeutic;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Macaque sp.
XX
PN   WO9733913-A1.
XX
PD   18-SEP-1997.
XX
PF   12-MAR-1997;   97WO-US04043.
```

```
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 0 C; 8 G; 4 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      15 ACTCCACTCACTCCA 1


RESULT   7
AAZ90893/c
ID   AAZ90893 standard; DNA; 15 BP.
XX
AC   AAZ90893;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #121.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 44; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 8 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      15 ACTCCACTCGCTCCA 1


RESULT   8
AAZ90894/c
ID   AAZ90894 standard; DNA; 16 BP.
XX
AC   AAZ90894;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #122.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 44; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 16 BP; 3 A; 0 C; 8 G; 5 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 16;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      16 ACTCCACTCACTCCA 2


RESULT   9
AAV27168
ID   AAV27168 standard; DNA; 18 BP.
XX
AC   AAV27168;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Haemopoietin receptor primer 2057.
XX
KW   Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
```

```
AC   AAZ90848;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #76.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 41; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 4 A; 0 C; 7 G; 4 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      15 ACTCCATTCACTCCA 1


RESULT   5
AAZ90864/c
ID   AAZ90864 standard; DNA; 15 BP.
XX
AC   AAZ90864;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #92.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 42; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 8 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTCRCTCCA 15
           :|||||:||:|||||
Db      15 GCTCCACTCACTCCA 1


RESULT   6
AAZ90880/c
ID   AAZ90880 standard; DNA; 15 BP.
XX
AC   AAZ90880;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #108.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
```

```
PS   Claim 12; Page 51; 87pp; English.
XX
CC   5 Degenerate hybridisation probes (AAT17870-74) are based on a
CC   conserved motif (AAR92812) found in haemopoietin receptors.  The
CC   probes are used in the identification and/or cloning of genes
CC   coding for novel haemopoietin receptors, e.g. the murine
CC   interleukin-11 (IL-11) receptor alpha chain gene (AAT17868).  Such
CC   receptors are defined by their ability to hybridise to the
CC   probes under medium stringency conditions.
XX
SQ   Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;


  Query Match             92.0%;  Score 13.8;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          |||||||||||||||
Db      1 rctccaytcrctcca 15


RESULT   2
AAV27139
ID   AAV27139 standard; DNA; 15 BP.
XX
AC   AAV27139;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Novel haemopoietin receptor probe 2.
XX
KW   Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW   cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW   probe.
XX
OS   Synthetic.
OS   Mammalian.
XX
PN   WO9811225-A2.
XX
PD   19-MAR-1998.
XX
PF   11-SEP-1997;   97WO-GB02479.
XX
PR   11-SEP-1996;   96AU-0002246.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PA   (DZIE/) DZIEGLEWSKA H E.
XX
PI   Alexander W,  Fabri L,  Farley A,  Hilton DJ,  Kikuchi Y;
PI   Kojima T,  Maeda M,  Nash A,  Nicola NA,  Rakar S,  Willson T;
PI   Zhang J;
XX
DR   WPI; 1998-260970/23.
XX
PT   New isolated haemopoietin receptor - used for developing products
PT   for modulating proliferation, differentiation and survival of cells,
PT   e.g. neuronal cells
XX
PS   Claim 3; Page 132; 182pp; English.
XX
CC   The probes AAV27138 and AAV27139 are used to identify nucleic acid
CC   molecules encoding a novel haemopoietin receptor (HR).  Interaction
CC   between the novel HR and a ligand facilitates proliferation,
CC   differentiation and survival of a wide variety of cells.  The HR and it's
CC   derivatives can be used for modulating the activity of the receptors e.g.
CC   to regulate development, maintenance or regeneration in an array of
CC   different cells and tissues in vitro and in vivo.  They can be present in
CC   therapeutics used for modulating neuronal proliferation, differentiation
CC   and survival. The products can also be used for detection and diagnosis,
CC   e.g. for cancers or predisposition to cancers, or for drug screening.
XX
SQ   Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;


  Query Match             92.0%;  Score 13.8;  DB 19;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          |||||||||||||||
Db      1 rctccaytcrctcca 15


RESULT   3
AAZ90830/c
ID   AAZ90830 standard; DNA; 15 BP.
XX
AC   AAZ90830;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #58.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 0 C; 8 G; 4 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTCRCTCCA 15
          :|||||:||:|||||
Db     15 ACTCCACTCACTCCA 1


RESULT   4
AAZ90848/c
ID   AAZ90848 standard; DNA; 15 BP.
XX
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 18:12:59 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-6
Perfect score: 15
Sequence: 1 RCTCCAYTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /SIDS8/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13.8	92.0	15	17	AAT17870	Haemopoietin recep
2		13.8	92.0	15	19	AAV27139	Novel haemopoietin
c 3		13.8	92.0	15	21	AAZ90830	Human NR8 gene pro
c 4		13.8	92.0	15	21	AAZ90848	Human NR8 gene pro
c 5		13.8	92.0	15	21	AAZ90864	Human NR8 gene pro
c 6		13.8	92.0	15	21	AAZ90880	Human NR8 gene pro
c 7		13.8	92.0	15	21	AAZ90893	Human NR8 gene pro
c 8		13.8	92.0	16	21	AAZ90894	Human NR8 gene pro
9		13.8	92.0	18	19	AAV27168	Haemopoietin recep
c 10		13.8	92.0	21	22	AAF95960	Human gene single
c 11		13.8	92.0	25	18	AAT96787	Human and macaque
c 12		13.8	92.0	71	21	AAA61554	Human IL-5R alpha
c 13		13.8	92.0	330	21	AAZ59255	Fragment of mouse
c 14		13.8	92.0	444	21	AAA89731	Mouse IL-3 recepto
c 15		13.8	92.0	465	19	AAV22698	Interleukin-13 bin
c 16		13.8	92.0	657	21	AAZ94555	Cytokine receptor
c 17		13.8	92.0	690	16	AAT04952	Interleukin 4 comp
c 18		13.8	92.0	693	15	AAQ54831	IL-2 receptor gamm
c 19		13.8	92.0	696	18	AAV04437	Interleukin 4 rece
c 20		13.8	92.0	759	15	AAQ54830	IL-2 receptor gamm
21		13.8	92.0	807	10	AAN90793	Clone cMZ-8 encodi
c 22		13.8	92.0	870	21	AAZ50746	HUMAN Orphan Cytok
c 23		13.8	92.0	907	21	AAZ59253	Human NR8gamma 3'
c 24		13.8	92.0	931	21	AAF20982	Human low adenosin
c 25		13.8	92.0	931	21	AAA34860	Human adenosine re
c 26		13.8	92.0	938	19	AAV27142	Novel haemopoietin
c 27		13.8	92.0	938	21	AAA46793	DNA encoding a mur
c 28		13.8	92.0	947	19	AAV22702	Mature interleukin
c 29		13.8	92.0	975	21	AAA70701	Human interleukin
c 30		13.8	92.0	1035	21	AAZ40288	SR345 coding seque
c 31		13.8	92.0	1044	15	AAQ54829	IL-2 receptor gamm
c 32		13.8	92.0	1074	18	AAV04440	Interleukin 6 rece
c 33		13.8	92.0	1079	19	AAV22701	Construct containi
c 34		13.8	92.0	1126	18	AAT96784	Celebus macaque Zc
c 35		13.8	92.0	1128	21	AAZ59247	Human NR8alpha/TPO
c 36		13.8	92.0	1167	18	AAT96783	Human Zcytor2 cyto
c 37		13.8	92.0	1188	13	AAQ22974	Sequence of the op
c 38		13.8	92.0	1218	20	AAZ06347	Nucleotide sequenc
c 39		13.8	92.0	1218	21	AAZ50346	Mouse orphan cytok
c 40		13.8	92.0	1229	21	AAZ94577	Mouse cytokine rec
c 41		13.8	92.0	1233	20	AAZ08861	Human DNAX soluble
c 42		13.8	92.0	1260	13	AAQ22972	Sequence encoding
c 43		13.8	92.0	1260	20	AAZ09202	Human IL-6 recepto
c 44		13.8	92.0	1281	20	AAX89654	cDNA encoding a hu
c 45		13.8	92.0	1288	19	AAV04131	Human HR-1 recepto

ALIGNMENTS

RESULT 1
AAT17870
ID AAT17870 standard; DNA; 15 BP.
XX
AC AAT17870;
XX
DT 21-MAY-1996 (first entry)
XX
DE Haemopoietin receptor probe HYB1.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN WO9607737-A1.
XX
PD 14-MAR-1996.
XX
PF 05-SEP-1995; 95WO-AU00578.
XX
PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ;
XX
DR WPI; 1996-171612/17.
XX
PT Nucleic acid encoding haemopoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists
XX

Search completed: August 29, 2001, 19:51:58
Job time: 17236 sec

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          denervated skeletal muscle
  JOURNAL   J. Neurochem. 65 (6), 2393-2400 (1995)
  MEDLINE   96064819
REFERENCE   2  (bases 1 to 1089)
  AUTHORS   Ip,N.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-1995) Nancy Y. Ip, Department of Biology, The
            Hong Kong University of Science and Technology, Clear Water Bay,
            Kowloon, Hong Kong
FEATURES             Location/Qualifiers
     source          1. .1089
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
                     /tissue_type="brain"
                     /dev_stage="embryo"
     CDS             1. .1089
                     /note="CNTF receptor alpha component"
                     /codon_start=1
                     /product="ciliary neurotrophic factor receptor alpha
                     component"
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                     /db_xref="GI:1151069"
                     /translation="MANPVPSACCVVLAAVVVVYAQRHSQQDSHIQYERVGADVTMKC
                     GSMDWDAAVTWTANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSSWHLKYQTYLR
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                     RCHIRYLQLFSTVKYKVTLTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPR
                     RLEVSWQNPSSWPDPESFPLKFFLRYRPLILDQWQHVELSDGTSHTITDAYAGKEYII
                     QVAAKDNDIGTWSDWSVAVHATPWTEEPKHLTTEVQITETTSTSTSSFMPPPTTKICD
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BASE COUNT      245 a    341 c    294 g    209 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 8;  Length 1089;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    876 ACTCCAGTCGCTCCA 862


RESULT  14
HLPR108/c
LOCUS       HLPR108      1218 bp    DNA             PRI       02-OCT-1996
DEFINITION  Human leptin receptor (LEPR) gene, exon 8.
ACCESSION   U59253
VERSION     U59253.1  GI:1589760
KEYWORDS    .
SEGMENT     8 of 18
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1218)
  AUTHORS   Thompson,D.B., Ossowski,V., Sutherland,J., Apel,W. and
            Biesterfeldt,J.
  TITLE     Human Leptin Receptor
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1218)
  AUTHORS   Thompson,D.B., Ossowski,V., Sutherland,J., Apel,W. and
            Biesterfeldt,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAY-1996) Clinical Diabetes and Nutrition Section,
            National Institutes of Health, 4212 N. 16th Street, Phoenix, AZ
            85016, USA
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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     exon            550. .694
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                     /number=8
BASE COUNT      335 a    211 c    223 g    430 t     19 others
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 8.6e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    669 ACTCCAGTCACTCCA 655


RESULT  15
AF329103/c
LOCUS       AF329103     1227 bp    DNA             PLN       29-JAN-2001
DEFINITION  Stachybotrys chartarum trichodiene synthase (TRI5) gene, complete
            cds.
ACCESSION   AF329103
VERSION     AF329103.1  GI:12584944
KEYWORDS    .
SOURCE      Stachybotrys chartarum.
  ORGANISM  Stachybotrys chartarum
            Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
REFERENCE   1  (bases 1 to 1227)
  AUTHORS   Peplow,A.W. and Beremand,M.N.
  TITLE     Putative trichothecene genes of Stachybotrys chartarum
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1227)
  AUTHORS   Peplow,A.W. and Beremand,M.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-2000) Department of Plant Pathology &
            Microbiology, Texas A&M University, 2132 TAMUS, College Station, TX
            77843-2132, USA
FEATURES             Location/Qualifiers
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                     /organism="Stachybotrys chartarum"
                     /strain="JS58-17"
                     /db_xref="taxon:74722"
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                     /product="trichodiene synthase"
     gene            <1. .>1227
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                     /gene="TRI5"
                     /codon_start=1
                     /product="trichodiene synthase"
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                     /db_xref="GI:12584945"
                     /translation="MEAFPTEYFLGTAVRLLENVKYRDSNYTREERVENLQYAYNKAA
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                     CWIEQYNFHGFPGSFDYPGFLRRMNGLGHCVGGSLWPKENFNEQEHFLEITSAIAQME
                     NWMVWVNDLMSFYKEFDDPRDQTSLVKNYVVSEGITLNQALEKLTQDTLQSSEQMMVV
                     FSQKDPKIMDTIECFMHGYITWHLCDNRYRLKEIYDRTKDIQTEDAMKFRKFYEQAFK
                     VGAIEATEWAYPTVVERLEQRKAEEQAERDEQAALANPEKAQVAQVVLA"
BASE COUNT      321 a    326 c    316 g    264 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 13;  Length 1227;
  Best Local Similarity   80.0%;  Pred. No. 8.6e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db   1135 GCTCCAATCGCTCCA 1121
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            8-10, complete cds.
ACCESSION   L38025
VERSION     L38025.1  GI:608654
KEYWORDS    ciliary neurotrophic factor alpha receptor.
SEGMENT     6 of 6
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Valenzuela,D.M., Rojas,E., Le Beau,M.M., Espinosa,R., Brannan,C.I.,
            McClain,J., Masiakowski,P., Ip,N.Y., Copeland,N.G., Jenkins,N.A.
            and Yancopoulos,G.D.
  TITLE     Genomic organization and chromosomal localization of the human and
            mouse genes encoding the alpha receptor component for ciliary
            neurotrophic factor
  JOURNAL   Genomics 25 (1), 157-163 (1995)
  MEDLINE   95293367
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                     L38023.1:26. .259,L38024.1:26. .144,L38024.1:319. .484,
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     CDS             join(L38022.1:26. .110,L38023.1:26. .259,L38024.1:26. .144,
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                     809)
                     /codon_start=1
                     /product="ciliary neurotrophic factor alpha receptor"
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                     /translation="MAAPVPWACCAVLAAAAAVVYAQRHSPQEAPHVQYERLGSDVTL
                     PCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLRHQVL
                     LHVGLPPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIMVCEKDPAL
                     KNRCHIRYMHLFSTIKYKVSISVSNALGHNATAITFDEFTIVKPDPPENVVARPVPSN
                     PRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHVELSDGTAHTITDAYAGKEY
                     IIQVAAKDNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKI
                     CDPGELGSGGGPSAPFLVSVPITLALAAAAATASSLLI"
     exon            26. .206
                     /number=8
     exon            551. .719
                     /number=9
     exon            809. .993
                     /note="non-coding exon"
                     /number=10
BASE COUNT      177 a    336 c    292 g    188 t
ORIGIN
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  Query Match             92.0%;  Score 13.8;  DB 97;  Length 993;
  Best Local Similarity   80.0%;  Pred. No. 8.5e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    139 GCTCCAGTCACTCCA 125
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RESULT  12
E11420/c
ID   E11420     standard; RNA; HUM; 999 BP.
XX
AC   E11420;
XX
SV   E11420.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   cDNA encoding Ig-CRH region of human G-CSF receptor.
XX
KW   JP 1996140678-A/2.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-999
RA   Ota Y., Hiraoka O., Anaguchi H.;
RT   "DNA CODING FOR PROTEIN OF LIGAND-BONDING REGION CONTAINING CRH REGION OF
RT   GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR";
RL   Patent number JP1996140678-A/2, 04-JUN-1996.
RL   TANPAKU KOGAKU KENKYUSHO:KK.
XX
CC   OS   Homo sapiens (human)
CC   PN   JP 1996140678-A/2
CC   PD   04-JUN-1996
CC   PF   15-NOV-1994 JP 1994280655
CC   PI   OTA YOSHIMI, HIRAOKA OSAMU, ANAGUCHI HIROYUKI
CC   PC   C12N15/09,C07H21/04,C07K14/715,C12N5/10,C12P21/02,(C12N5/10,
CC   PC   C12R1:91),
CC   PC   (C12P21/02,C12R1:91);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .999
CC   FT                   /organism="Homo sapiens"
CC   FT                   /tissue_type="placenta"
CC   FT   sig_peptide     1. .69
CC   FT                   /product="signal peptide of G-CSF receptor"
CC   FT   mat_peptide     70. .999
CC   FT                   /product="Ig-CRH region of G-CSF receptor"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .999
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
XX
SQ   Sequence 999 BP; 207 A; 347 C; 276 G; 169 T; 0 other;
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  Query Match             92.0%;  Score 13.8;  DB 45;  Length 999;
  Best Local Similarity   80.0%;  Pred. No. 8.5e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    966 GCTCCAGTCGCTCCA 952
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RESULT  13
GGU29245/c
LOCUS       GGU29245     1089 bp    mRNA            VRT       16-FEB-1996
DEFINITION  Gallus gallus ciliary neurotrophic factor receptor alpha component
            mRNA, complete cds.
ACCESSION   U29245
VERSION     U29245.1  GI:1151068
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1089)
  AUTHORS   Ip,F.C., Fu,A.K., Tsim,K.W. and Ip,N.Y.
  TITLE     Cloning of the alpha component of the chick ciliary neurotrophic
            factor receptor: developmental expression and down-regulation in
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CC   FT   misc_feature    1. .639
CC   FT                  /note="CRH region of G-CSF receptor"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .639
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
XX
SQ   Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 45;  Length 639;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     606 GCTCCAGTCGCTCCA 592


RESULT   9
E11371/c
ID   E11371     standard; RNA; HUM; 639 BP.
XX
AC   E11371;
XX
SV   E11371.1
XX
DT   07-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   cDNA encoding CRH region of human G-CSF receptor.
XX
KW   JP 1996131172-A/2.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-639
RA   Ota Y., Anaguchi H.;
RT   "DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
RT   STIMULATING FACTOR RECEPTOR";
RL   Patent number JP1996131172-A/2, 28-MAY-1996.
RL   TANPAKU KOGAKU KENKYUSHO:KK.
XX
CC   OS   Homo sapiens (human)
CC   PN   JP 1996131172-A/2
CC   PD   28-MAY-1996
CC   PF   14-NOV-1994 JP 1994278841
CC   PI   OTA YOSHIMI, ANAGUCHI HIROYUKI
CC   PC   C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
CC   PC   C12R1:19),
CC   PC   (C12P21/02,C12R1:19);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .639
CC   FT                   /organism="Homo sapiens"
CC   FT                   /cell_line="U937"
CC   FT                   /tissue_type="placenta"
CC   FT   mat_peptide     1. .639
CC   FT                   /product="CRH region of human G-CSF receptor"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .639
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
XX
SQ   Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 45;  Length 639;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     606 GCTCCAGTCGCTCCA 592


RESULT  10
MUMULEPR06/c
LOCUS       MUMULEPR06    801 bp    DNA             ROD       09-JAN-1998
DEFINITION  Mus musculus leptin receptor (Lepr) gene, exon 6.
ACCESSION   AF039448
VERSION     AF039448.1  GI:2760934
KEYWORDS    .
SEGMENT     6 of 19
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Chua,S.C., Chung,W.K., Wu-Peng,X.S., Zhang,Y., Liu,S.M.,
            Tartaglia,L. and Leibel,R.L.
  TITLE     Phenotypes of mouse diabetes and rat fatty due to mutations in the
            OB (leptin) receptor
  JOURNAL   Science 271 (5251), 994-996 (1996)
  MEDLINE   96172360
REFERENCE   2  (bases 1 to 801)
  AUTHORS   Chua,S.C., Koutras,I.K., Han,L., Liu,S.M., Kay,J., Young,S.J.,
            Chung,W.K. and Leibel,R.L.
  TITLE     Fine structure of the murine leptin receptor gene: splice site
            suppression is required to form two alternatively spliced
            transcripts
  JOURNAL   Genomics 45 (2), 264-270 (1997)
  MEDLINE   98008913
REFERENCE   3  (bases 1 to 801)
  AUTHORS   Chua,S.C., Koutras,I.K., Han,L., Liu,S.M., Kay,J., Young,S.J.,
            Chung,W.K. and Leibel,R.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-1997) Pediatrics, Columbia University, 1150 St.
            Nicholas Avenue, New York, NY 10032, USA
FEATURES             Location/Qualifiers
     source          1. .801
                     /organism="Mus musculus"
                     /strain="129/J"
                     /db_xref="taxon:10090"
                     /chromosome="4"
     exon            300. .444
                     /gene="Lepr"
                     /number=6
BASE COUNT      188 a    143 c    199 g    270 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 94;  Length 801;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     419 ACTCCAGTCACTCCA 405


RESULT  11
HUMCNFAR06/c
LOCUS       HUMCNFAR06    993 bp    DNA             PRI       09-JAN-2001
DEFINITION  Homo sapiens ciliary neurotrophic factor alpha receptor gene, exons
```

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  MEDLINE   97224611
REFERENCE   2  (bases 1 to 597)
  AUTHORS   Coleman,A.W. and Mai,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-1996) BioMed, Brown University, Providence, RI
            02912, USA
COMMENT     On Nov 20, 1997 this sequence version replaced gi:2039187.
FEATURES             Location/Qualifiers
     source          1. .597
                     /organism="Chlamydomonas incerta"
                     /strain="SAG7.73"
                     /db_xref="taxon:51695"
     misc_RNA        1. .199
                     /note="ITS1"
                     /product="internal transcribed spacer 1"
     rRNA            200. .358
                     /product="5.8S ribosomal RNA"
     misc_RNA        359. .597
                     /note="ITS2"
                     /product="internal transcribed spacer 2"
BASE COUNT      157 a    156 c    142 g    142 t
ORIGIN


  Query Match.             92.0%;  Score 13.8;  DB 14;  Length 597;
  Best Local Similarity    80.0%;  Pred. No. 8.2e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    399 GCTCCAATCACTCCA 385


RESULT   7
G56634/c
LOCUS       G56634         620 bp    DNA             STS       30-MAR-2000
DEFINITION  SHGC-102031 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G56634
VERSION     G56634.1  GI:6121803
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Olivier,M. and Cox,D.R.
  TITLE     Unpublished, Olivier, M., Cox, D.R. (2000)
  JOURNAL   Unpublished (2000)
COMMENT
            Contact: Michael Olivier, David R. Cox
            Stanford Human Genome Center
            Stanford University School of Medicine
            4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
            Tel: (650) 320-5800
            Fax: (650) 320-5801
            Email: olivier@shgc.stanford.edu
            Primer A: TTTCCTGCTGTTCTTTGTCCAAT
            Primer B: GATTTCATCAGGTCCAGCAATTC
            STS size: 281
            PCR Profile:
                    Initial incubation: 95 degrees C for 10 minutes
                    Denaturation:       94 degrees C for 30 seconds
                    Annealing:          60 degrees C for 30 seconds
                    Polymerization:     72 degrees C for 23 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9700
            Protocol:
                    Template:                   25 ng
                    Primer:                     each 1 uM
                    dNTPs:                      each 200 uM
                    AmpliTaq Gold Polymerase:   0.07 units/ul
                    Total Vol:                  5 ul
            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50 mM
                    Tris-HCl:       10 mM
                    pH:             8.3

            BAC ends sequenced at TIGR from the RPCI11 BAC library. Designed
            and developed at the Stanford Human Genome Center.
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="11"
                     /clone_lib="Human"
     STS             267. .547
     primer_bind     267. .289
     primer_bind     complement(525. .547)
BASE COUNT      157 a    123 c    147 g    193 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 54;  Length 620;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    151 GCTCCAATCACTCCA 137


RESULT   8
E09857/c
ID   E09857 ·  standard; RNA; HUM; 639 BP.
XX
AC   E09857;
XX
SV   E09857.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   cDNA encoding CRH region of G-CSF receptor.
XX
KW   JP 1995227288-A/2.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-639
RA   Ota Y., Anaguchi H., Hiraoka O.;
RT   "DNA CODING FOR LIGAND BOND RANGE PROTEIN OF GRANULOCYTE COLONY STIMULATION
RT   FACTOR RECEPTOR";
RL   Patent number JP1995227288-A/2, 29-AUG-1995.
RL   TANPAKU KOGAKU KENKYUSHO:KK.
XX
CC   OS   Homo sapiens (human)
CC   PN   JP 1995227288-A/2
CC   PD   29-AUG-1995
CC   PF   30-MAY-1994 JP 1994116252
CC   PR   21-DEC-1993 JP 93P   321862
CC   PI   OTA YOSHIMI, ANAGUCHI HIROYUKI, HIRAOKA OSAMU
CC   PC   C12N15/09,C12P21/02,(C12N15/09,C12R1:91),(C12P21/02,C12R1:19);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .639
CC   FT                   /organism="Homo sapiens"
CC   FT                   /tissue_type="Placenta"
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   PUBMED   9699267
REFERENCE   3  (bases 1 to 373)
  AUTHORS   van der Poel,J.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAR-1997) Animal Breeding, Agricultural University
            Wageningen, Marijikeweg 40, Wageningen 6708 PG, The Netherlands
COMMENT     GSDB:S:48171.
            [Flatfile retrieved from GSDB Fri Feb 23 09:21:05 2001].
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Gallus gallus"
                     /db_xref="taxon:9031"
                     /clone="cDNA42R"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /note="derived from cDNA library".
     repeat_region   1. .373
                     /note="microsatellite MCW111"
                     /rpt_type=tandem
BASE COUNT      140 a     74 c     53 g    102 t      4 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 8;  Length 373;
  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    307 ACTCCAATCACTCCA 321


RESULT   4
S47134S6/c
LOCUS       S47134S6      387 bp                    INV       08-MAY-1993
DEFINITION  unc-5=immunoglobulin and thrombospondin type 1 transmembrane
            protein {alternatively spliced} [Caenorhabditis elegans, variety
            Bergerac, Genomic/mRNA, 387 nt, segment 6 of 9].
ACCESSION   S47165
VERSION     S47165.1  GI:258524
KEYWORDS    .
SEGMENT     6 of 9
SOURCE      Caenorhabditis elegans variety Bergerac.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Leung-Hagesteijn,C., Spence,A.M., Stern,B.D., Zhou,Y., Su,M.W.,
            Hedgecock,E.M. and Culotti,J.G.
  TITLE     UNC-5, a transmembrane protein with immunoglobulin and
            thrombospondin type 1 domains, guides cell and pioneer axon
            migrations in C. elegans
  JOURNAL   Cell 71 (2), 289-299 (1992)
  MEDLINE   93046629
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 116678] from the original journal article.
            This sequence comes from Fig. 2.
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Caenorhabditis elegans"
                     /db_xref="taxon:6239"
                     /variety="Bergerac"
BASE COUNT      106 a     84 c    107 g     90 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 96;  Length 387;
  Best Local Similarity   80.0%;  Pred. No. 8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    261 ACTCCAATCACTCCA 247


RESULT   5
AF227555/c
LOCUS       AF227555      457 bp    mRNA            PRI       01-JUN-2000
DEFINITION  Macaca mulatta interleukin-6 signal transducer receptor (IL-6)
            mRNA, partial cds.
ACCESSION   AF227555
VERSION     AF227555.1  GI:8132802
KEYWORDS    .
SOURCE      rhesus monkey.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Arredondo,J.
  TITLE     Cytokine Signal Transduction Genes from Rhesus Macaques
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 457)
  AUTHORS   Arredondo,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) California Regional Primate Research
            Center, University of California-Davis, One Shields Avenue, Davis,
            CA 95616, USA
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Macaca mulatta"
                     /db_xref="taxon:9544"
                     /cell_type="peripheral blood mononuclear cells"
     gene            <1. .>457
                     /gene="IL-6"
                     /note="gp130"
     CDS             <1. .>457
                     /gene="IL-6"
                     /note="membrane glycoprotein"
                     /codon_start=2
                     /product="interleukin-6 signal transducer receptor"
                     /protein_id="AAF73398.1"
                     /db_xref="GI:8132803"
                     /translation="PAEDTASTRSSFTVQDLKPFTEYVFRICCMKEDGKGYWSDWSEE
                     ANGITYEDRPSKAPSFWYKIDPSHAQGYRTVQLMWKTLPPFEANGKILDYEVTLTRWK
                     SHLQNYTVNDTKLTVNLTNDRYVATLTARNLVGKSDAAVLTIPACDFQAT"
BASE COUNT      155 a     93 c     88 g    121 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 89;  Length 457;
  Best Local Similarity   80.0%;  Pred. No. 8.1e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    127 ACTCCAGTCACTCCA 113


RESULT   6
CIU66950/c
LOCUS       CIU66950      597 bp    DNA             PLN       20-NOV-1997
DEFINITION  Chlamydomonas incerta internal transcribed spacer 1, 5.8S ribosomal
            RNA gene; and internal transcribed spacer 2, complete sequence.
ACCESSION   U66950
VERSION     U66950.1  GI:2627277
KEYWORDS    .
SOURCE      Chlamydomonas incerta.
  ORGANISM  Chlamydomonas incerta
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 597)
  AUTHORS   Mai,J.C. and Coleman,A.W.
  TITLE     The internal transcribed spacer 2 exhibits a common secondary
            structure in green algae and flowering plants
  JOURNAL   J. Mol. Evol. 44 (3), 258-271 (1997)
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c	9	13.8	92.0	639	45	E11371 E11371 cDNA encodi
c	10	13.8	92.0	801	94	MUMULEPR06 AF039448 Mus muscu
c	11	13.8	92.0	993	97	HUMCNFAR06 L38025 Homo sapien
c	12	13.8	92.0	999	45	E11420 E11420 cDNA encodi
c	13	13.8	92.0	1089	8	GGU29245 U29245 Gallus gall
c	14	13.8	92.0	1218	91	HLPR108 U59253 Human lepti
c	15	13.8	92.0	1227	13	AF329103 AF329103 Stachybot
c	16	13.8	92.0	1248	8	GGGPARA Z48168 G.gallus mR
c	17	13.8	92.0	1332	95	S54212 S54212 ciliary neu
c	18	13.8	92.0	1423	5	AF133269 AF133269 Drosophil
c	19	13.8	92.0	1514	12	AF053926 AF053926 Stachybot
c	20	13.8	92.0	1566	97	HUMCNTFR M73238 Human cilia
c	21	13.8	92.0	1591	9	AR066232 AR066232 Sequence
c	22	13.8	92.0	1591	9	AR070290 AR070290 Sequence
c	23	13.8	92.0	1591	9	AR074863 AR074863 Sequence
c	24	13.8	92.0	1591	10	I12552 I12552 Sequence 1
c	25	13.8	92.0	1591	10	I56052 I56052 Sequence 1
	26	13.8	92.0	1593	7	OCU09028 U09028 Oryctolagus
c	27	13.8	92.0	1680	95	S80963 S80963 NR4=IL-13 r
c	28	13.8	92.0	1707	10	I50845 I50845 Sequence 2
c	29	13.8	92.0	1878	85	AB015706 AB015706 Homo sapi
c	30	13.8	92.0	1975	94	AF068615 AF068615 Mus muscu
c	31	13.8	92.0	1977	9	A49472 A49472 Sequence 1
c	32	13.8	92.0	1977	9	AR079661 AR079661 Sequence
c	33	13.8	92.0	2272	8	AF041846 AF041846 Xenopus l
c	34	13.8	92.0	2369	9	AR019619 AR019619 Sequence
c	35	13.8	92.0	2369	9	AR070271 AR070271 Sequence
c	36	13.8	92.0	2416	94	AB012290 AB012290 Mus muscu
c	37	13.8	92.0	2418	94	MMU49110 U49110 Mus musculu
c	38	13.8	92.0	2460	94	BC005707 BC005707 Mus muscu
c	39	13.8	92.0	2466	5	AF135119 AF135119 Drosophil
c	40	13.8	92.0	2469	94	MMAJ4115 AJ224115 Mus muscu
c	41	13.8	92.0	2502	94	MUSSDFLIFR D17444 Mouse mRNA
c	42	13.8	92.0	2546	93	HSGCSFRD X55720 Human mRNA
c	43	13.8	92.0	2547	7	AF167719 AF167719 Sus scrof
c	44	13.8	92.0	2644	7	BTA308426 AJ308426 Bos tauru
	45	13.8	92.0	2647	89	AK022852 AK022852 Homo sapi

ALIGNMENTS

```
RESULT   1
A70377
LOCUS       A70377          15 bp    DNA             PAT       07-MAY-1999
DEFINITION  Sequence 7 from Patent WO9811225.
ACCESSION   A70377
VERSION     A70377.1  GI:4774658
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
            Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
            Kikuchi,Y.
  TITLE     A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
  JOURNAL   Patent: WO 9811225-A 7 19-MAR-1998;
            NICOLA NICOS ANTONY (AU)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      7 c      0 g      3 t      3 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           |||||||||||||||
Db       1 RCTCCARTCRCTCCA 15


RESULT   2
HSJ10F12/c
LOCUS       HSJ10F12        340 bp    DNA             STS       07-MAR-2000
DEFINITION  STS from H.sapiens random shear fragment, sequence tagged site.
ACCESSION   AL159451
VERSION     AL159451.1  GI:7210385
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Hunt,S., Sims,S., Willey,D., Carter,N. and Ross,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2000) E-mail contact: humquery@sanger.ac.uk
COMMENT     Marker stSG67529 (Primer A : AAAAGTGAAAGAAGGGGAAAGG; Primer B :
            GATAACCCAAGCGCATGG; amplimer size : 141 bp) was developed from a
            single pass sequencing read from H.sapiens flow-sorted chromosome
            9-12 random shear fragment, SC9-12pJ10F12. Vector : pUC18 Site :
            SmaI
            Further information : http://www.sanger.ac.uk/HGP/Chr10/.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /sex="male"
                     /clone="SC9-12pJ10F12"
                     /tissue_type="Lymphoblastoid cell line"
                     /clone_lib="SC9-12pJ"
BASE COUNT      131 a     44 c     77 g     87 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 54;  Length 340;
  Best Local Similarity   80.0%;  Pred. No. 7.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db      48 GCTCCAGTCACTCCA 34


RESULT   3
L48909
LOCUS       L48909          373 bp    mRNA            VRT       23-FEB-2001
DEFINITION  Gallus gallus clone cDNA42R microsatellite MCW111 sequence.
ACCESSION   L48909
VERSION     L48909.1  GI:13111695
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Ruyter-Spira,C.P., Crooijmans,R.P., Dijkhof,R.J., van Oers,P.A.,
            Strijk,J.A., van der Poel,J.J. and Groenen,M.A.
  TITLE     Development and mapping of polymorphic microsatellite markers
            derived from a chicken brain cDNA library
  JOURNAL   Anim. Genet. 27 (4), 229-234 (1996)
  MEDLINE   97009815
   PUBMED   8856919
REFERENCE   2  (bases 1 to 373)
  AUTHORS   Ruyter-Spira,C.P., de Koning,D.J., van der Poel,J.J.,
            Crooijmans,R.P., Dijkhof,R.J. and Groenen,M.A.
  TITLE     Developing microsatellite markers from cDNA: a tool for adding
            expressed sequence tags to the genetic linkage map of the chicken
  JOURNAL   Anim. Genet. 29 (2), 85-90 (1998)
  MEDLINE   98364423
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:51:55 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-7
Perfect score: 15
Sequence: 1 RCTCCARTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
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42: em_om:*
43: em_or:*
44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
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93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13.8	92.0	15	9	A70377	A70377 Sequence 7
2	c	13.8	92.0	340	54	HSJ10F12	AL159451 STS from
3		13.8	92.0	373	8	L48909	L48909 Gallus gall
4	c	13.8	92.0	387	96	S47134S6	S47165 unc-5=immun
5	c	13.8	92.0	457	89	AF227555	AF227555 Macaca mu
6	c	13.8	92.0	597	14	CIU66950	U66950 Chlamydomon
7	c	13.8	92.0	620	54	G56634	G56634 SHGC-102031
8	c	13.8	92.0	639	45	E09857	E09857 cDNA encodi

XX
PF 27-MAR-1998; 98WO-US06056.
XX
PR 28-MAR-1997; 97US-0042849.
XX
PA (CYTO-) CYTOCLONAL PHARM INC.
XX
PI Labidi AH;
XX
DR WPI; 1998-568277/48.
XX
PT Recombinant non-pathogenic Mycobacterium as vaccines providing long
PT term cellular immunity - useful against intracellular pathogens,
PT cancer and autoimmune disease, and are retained in host macrophages
XX
PS Disclosure; Fig 6; 120pp; English.
XX
CC This genomic DNA sequence is a fragment of the Mycobacterium fortiutum
CC plasmid pAL 5000 which contains ORF2. This sequence is used in a
CC method which results in the formation of Mycobacterium recombinant
CC vaccines from compositions that provide a continuous source of protein to
CC an animal and stimulate cellular immunity. Such compositions are used to
CC stimulate cellular immunity (by inducing Th-1 cells or cytotoxic T
CC lymphocytes), particularly as vaccines (live or dead) for treating and
CC preventing diseases caused by intracellular pathogens (bacteria, viruses,
CC rickettsia or protozoa), and also cancer, autoimmune diseases, allergy
CC and bovine spongiform encephalitis, in humans or animals. The vaccines
CC are administered by injection, orally and nasally. These compositions
CC provide consistent and long-lasting immunity. Transformed cells used in
CC the method are retained within macrophages, blocking the killing
CC mechanism but producing protective immunogen which is processed and
CC presented by the macrophage. Several immunogens may be included in the
CC same vaccine and the Mycobacterium cells serve as adjuvant.
XX
SQ Sequence 2096 BP; 348 A; 743 C; 670 G; 335 T; 0 other;

Query Match 92.0%; Score 13.8; DB 19; Length 2096;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 RCTCCARTCRCTCCA 15
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Db    1481 gctccaatcgctcca 1495
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  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db   1170 GCTCCAGTCACTCCA 1156


RESULT  13
AAQ83223/c
ID   AAQ83223 standard; cDNA; 1591 BP.
XX
AC   AAQ83223;
XX
DT   22-SEP-1995  (first entry)
XX
DE   Human recombinant mature CNTFR.
XX
KW   CNTFR; ciliary neurotrophic factor receptor; cytokine;
KW   agonist; antagonist; signal transduction pathway; pRPN151;
KW   Escherichia coli; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             289..1407
FT                   /*tag=  a
FT   mat_peptide     289..1404
FT                   /*tag=  b
XX
PN   WO9507467-A.
XX
PD   16-MAR-1995.
XX
PF   09-SEP-1994;   94WO-US10163.
XX
PR   09-SEP-1993;   93US-0118968.
XX
PA   (REGE-) REGENERON PHARM INC.
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Ihle JN,  Stahl N,  Yancopoulos GD;
XX
DR   WPI; 1995-123515/16.
DR   P-PSDB; AAR70147.
XX
PT   Detection of ciliary neurotrophic factor receptor agonists - by
PT   determination of levels of phosphorylation.
XX
PS   Disclosure; Fig.2a-2d; 125pp; English.
XX
CC   The gene encoding human CNTFR was subcloned into bacterial
CC   expression vector pCP110.  The resulting plasmid, pRPN151,
CC   encoded a recombinant, mature form of human CNTFR.  Further
CC   manipulation of the coding region optimized expression of the
CC   gene in E. coli RFJ26, allowing production of useful amounts
CC   of CNTFR.
XX
SQ   Sequence 1591 BP; 288 A; 538 C; 473 G; 292 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 16;  Length 1591;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db   1170 GCTCCAGTCACTCCA 1156


RESULT  14
AAT14602/c
ID   AAT14602 standard; DNA; 1977 BP.
XX
AC   AAT14602;
XX
DT   20-JUN-1996  (first entry)
XX
DE   Human gp130 splice variant gene.
XX
KW   Gp130; transmembrane domain; growth factor antagonist;
KW   embryo pre-implantation; in vitro fertilisation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9609382-A1.
XX
PD   28-MAR-1996.
XX
PF   21-SEP-1995;   95WO-GB02243.
XX
PR   21-SEP-1994;   94GB-0019021.
XX
PA   (ISTF ) ARS APPLIED RES SYST HOLDING NV.
XX
PI   Dellow KA,  Sharkey A,  Smith SK;
XX
DR   WPI; 1996-188444/19.
DR   P-PSDB; AAR94576.
XX
PT   New splice variant of gp130 lacking the trans-membrane domain  -
PT   useful as an antagonist for growth factors esp. for ensuring correct
PT   development of pre-implantation embryos
XX
PS   Example 2; Fig 1; 33pp; English.
XX
CC   A DNA sequence (AAT14602) codes for a novel splice variant (AAR94576) of
CC   human gp130.  The splice variant was initially detected during the
CC   morula to blastocyst transition stage of a human embryo.  The
CC   splicing event removes the exon coding for the transmembrane domain
CC   causing a frameshift resulting in a novel C-terminus (see AAR94575).
CC   The splice variant gp130 antagonises the action of certain growth
CC   factors and can be used to ensure correct development of
CC   preimplantation embryos, partic. for in vitro fertilisation.
XX
SQ   Sequence 1977 BP; 658 A; 396 C; 379 G; 544 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 17;  Length 1977;
  Best Local Similarity   80.0%;  Pred. No. 2e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    942 ACTCCAGTCACTCCA 928


RESULT  15
AAV69318
ID   AAV69318 standard; DNA; 2096 BP.
XX
AC   AAV69318;
XX
DT   01-FEB-1999  (first entry)
XX
DE   M. fortuitum plasmid pAL 5000 genomic DNA fragment.
XX
KW   Vaccine; cellular immunity; Th-1 cell; cancer; cytotoxic T lymphocyte;
KW   treatment; prevention; disease; autoimmune; intracellular pathogen; BSE;
KW   allergy; bovine spongiform encephalitis; macrophage; immunogen;
KW   adjuvant; ds.
XX
OS   Mycobacterium fortuitum.
XX
PN   WO9844096-A2.
XX
PD   31-OCT-1998.
```

```
CC   osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC   immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC   antidiabetic; hypotensive; dermatological; immunosuppressive;
CC   antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC   antithyroid; and antianaemic. The sequences can be used for determining
CC   the presence of or predisposition to, or preventing or treating
CC   pathological conditions associated with an ORFX-associated disorder. The
CC   nucleic acids can be used to express ORFX proteins in gene therapy
CC   vectors. The proteins and nucleic acids may be used to treat cancers,
CC   proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC   graft vs host disease, cardiovascular disease, diabetes mellitus,
CC   hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC   erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC   bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC   nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC   coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ   Sequence 1419 BP; 333 A; 436 C; 384 G; 265 T; 1 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 1419;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    545 gctccagtcactcca 559


RESULT  11
AAQ20195/c
ID   AAQ20195 standard; cDNA; 1591 BP.
XX
AC   AAQ20195;
XX
DT   31-MAR-1992  (first entry)
XX
DE   Ciliary neurotrophic factor receptor-coding sequence.
XX
KW   CNTFR; transgenic animal; motorneurone disease; trauma;
KW   muscular dystrophy; inflammation; amytrophic lateral sclerosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             289..1407
FT                   /*tag=  a
FT                   /product= CNTFR
XX
PN   WO9119009-A.
XX
PD   12-DEC-1991.
XX
PF   03-JUN-1991;   91WO-US03896.
XX
PR   15-MAY-1991;   91US-0700677.
PR   01-JUN-1990;   90US-0532285.
PR   28-MAR-1991;   91US-0676647.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Davis S,  Squinto S,  Furth M,  Yancopoulos GD;
XX
DR   WPI; 1992-007490/01.
DR   P-PSDB; AAR20024.
XX
PT   DNA encoding CNTF receptors - useful in diagnosis, physiological
PT   study and treatment of CNTF-related disorders
XX
PS   Claim 2; Fig 2; 92pp; English.
XX
CC   The CNTFR coding sequence can be incorporated into cells, cell lines
CC   and organisms (e.g. E.coli) for the expression of the receptor
CC   protein. Monoclonal antibodies can be raised to the CNTF. The cDNA
CC   can be used as a probe to screen a library for clones encoding
CC   members of the family of molecules including IL-6 receptor.
XX
SQ   Sequence 1591 BP; 289 A; 545 C; 465 G; 292 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 13;  Length 1591;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db   1170 GCTCCAGTCACTCCA 1156


RESULT  12
AAQ39626/c
ID   AAQ39626 standard; cDNA; 1591 BP.
XX
AC   AAQ39626;
XX
DT   30-SEP-1993  (first entry)
XX
DE   Sequence encoding human ciliary neurotrophic factor receptor (CNTF).
XX
KW   Ciliary neurotrophic factor; receptor; protein complex; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             289..1404
FT                   /*tag=  a
XX
PN   WO9311253-A.
XX
PD   10-JUN-1993.
XX
PF   01-DEC-1992;   92WO-US10632.
XX
PR   02-DEC-1991;   91US-0801562.
PR   09-APR-1992;   92US-0865878.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Aldrich TH,  Conover J,  Davis S,  Everdeen D,  Ip N;
PI   Nye SH,  Panayotatos N,  Squinto SP,  Stahl N,  Yancopoulos GD;
XX
DR   WPI; 1993-197070/24.
DR   P-PSDB; AAR37820.
XX
PT   Cell-free ciliary neurotrophic factor-receptor complex - for
PT   diagnosis and treatment of cell proliferation and differentiation
PT   disorders e.g. myeloid leukaemia
XX
PS   Disclosure; Fig 2; 122pp; English.
XX
CC   CNTF has been cloned and syntheisized in eukaryotic as well as
CC   bacterial expression systems, as described in International
CC   Application No. PCT/U.S. 90/05241. The CNTF receptor (CNTFR or CNTFR-
CC   alpha) has been cloned and expressed in eukaryotic cells, as
CC   described in U.S. Patent Application Serial No. 07/700,677 and
CC   International Application No. PCT/US91/03896, filed June 3, 1991.
CC   The present invention relates to a stable CNTF/receptor complex
CC   which possesses a different mobility in native polyacrylamide gels
CC   than either purified fractions of CNTF or CNTFR.
XX
SQ   Sequence 1591 BP; 289 A; 536 C; 473 G; 293 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 14;  Length 1591;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
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```
  Query Match             92.0%;  Score 13.8;  DB 15;  Length 1193;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    824 ACTCCAGTCACTCCA 810


RESULT   9
AAT66164/c
ID   AAT66164 standard; DNA; 1383 BP.
XX
AC   AAT66164;
XX
DT   15-JUL-1997  (first entry)
XX
DE   Mouse interleukin-12 receptor alpha chain NR4 DNA.
XX
KW   NR4; haemoprotein receptor; interleukin-13 receptor; IL-13;
KW   cytokine; allergy; asthma; therapy; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             61..1341
FT                   /*tag= a
FT   sig_peptide     61..141
FT                   /*tag= b
FT   mat_peptide     142..1338
FT                   /*tag= c
FT   misc_difference 121..123
FT                   /*tag= d
FT                   /note= "bases 121-123 (nnn) code for an
FT                         unidentified amino acid"
FT   misc_difference 640..642
FT                   /*tag= e
FT                   /note= "bases 640-642 (nnn) code for an
FT                         unidentified amino acid"
XX
PN   WO9715663-A1.
XX
PD   01-MAY-1997.
XX
PF   23-OCT-1996;   96WO-AU00668.
XX
PR   09-SEP-1996;   96AU-0002208.
PR   23-OCT-1995;   95AU-0006135.
PR   22-DEC-1995;   95AU-0007276.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Hilton DJ,  Metcalf D,  Nicola NA,  Willson T,  Zhang JG;
XX
DR   WPI; 1997-259018/23.
DR   P-PSDB; AAW09821.
XX
PT   DNA encoding animal haemopoietin receptor which interacts with
PT   interleukin-13 - useful to treat asthma, allergy or condition
PT   exacerbated by IgE production
XX
PS   Claim 6; Page 48-50; 93pp; English.
XX
CC   DNA sequences (AAT66164 and AAT66165) respectively code for novel mouse
CC   and human haemoprotein receptors (AAW09821 and AAW09822) designated NR4
CC   that comprise the interleukin-13 (IL-13) receptor alpha-chain.  To
CC   obtain the mouse sequence, genomic DNA prepd. from embryonal stem
CC   cells was screened with oligonucleotides encoding an amino acid
CC   sequence (WSDWS) found in many haemoprotein receptors.  The genomic
CC   clone was used isolate NR4 cDNA clones from WEHI-3B cells,
CC   peritoneal macrophage, bone marrow, skin and kidney libraries, and
CC   a composite sequence for mouse NR4 was produced.  The availability
CC   of genetic sequences for NR4 permits the development of a range of
CC   agents capable of modulating the activity of IL-13 and related
CC   cytokines such as interleukin-4 for the treatment of allergy, asthma
CC   and other conditions relating to IgE.  The genetic sequences can
CC   also be used in prodn. of recombinant NR4 or fusion proteins
CC   including NR4.
XX
SQ   Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T; 6 other;


  Query Match             92.0%;  Score 13.8;  DB 18;  Length 1383;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db   1050 ACTCCAATCACTCCA 1036


RESULT  10
AAC76452
ID   AAC76452 standard; cDNA; 1419 BP.
XX
AC   AAC76452;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF2007 polynucleotide sequence SEQ ID NO:4013.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US08621.
XX
PR   31-MAR-1999;   99US-0127607.
PR   02-APR-1999;   99US-0127636.
PR   05-APR-1999;   99US-0127728.
PR   30-MAR-2000; 2000US-0540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2000-602362/57.
DR   P-PSDB; AAB42243.
XX
PT   Novel nucleic acids and peptides derived from open reading frame X,
PT   useful for treating e.g. cancers, proliferative disorders,
PT   neurodegenerative disorders and cardiovascular disease -
XX
PS   Claim 5; Page 3192-3193; 5507pp; English.
XX
CC   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC   which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC   sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC   antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
```

```
PA   (KANF ) KANEKA CORP.
XX
PI   Kishimura M,  Nakao K,  Osakada F,  Osaki S,  Tanaka M;
XX
DR   WPI; 1997-281030/25.
DR   P-PSDB; AAW17859.
XX
PT   Auto-antigen from synovial cells of rheumatoid arthritis patients -
PT   binds to antibodies present in these patients, for diagnosis and
PT   prediction of the disease
XX
PS   Claim 9; Page 38; 61pp; Japanese.
XX
CC   The present sequence encodes the rheumatoid arthritis (RA)
CC   auto-antigen clone A, which can be used to diagnose and predict
CC   the development of RA by reaction with antibodies in biological
CC   specimens, e.g. sera, from patients.
CC   RNA was isolated from synovial cells from a RA patient and used to
CC   construct a cDNA library. This was screened using IgG separated
CC   from the synovial fluid of a RA patient. Active clones were
CC   isolated in a cloning vector, and inserted into an expression
CC   vector for the transformation of E. coli NM522. Transformants on
CC   culture express clone A peptide and follistatin related protein
CC   into the culture medium.
XX
SQ   Sequence 990 BP; 321 A; 190 C; 193 G; 286 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 18;  Length 990;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     942 ACTCCAGTCACTCCA 928


RESULT   7
AAT35138/c
ID   AAT35138 standard; DNA; 999 BP.
XX
AC   AAT35138;
XX
DT   30-OCT-1996  (first entry)
XX
DE   DNA encoding cytokine-receptor-complementary region G-CSF receptor.
XX
KW   G-CSF; granulocyte colony stimulating factor; receptor; leukaemia;
KW   over-proliferation; recombinant; vector; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..999
FT                   /*tag=  a
FT                   /note= "no stop codon"
XX
PN   JP08140678-A.
XX
PD   04-JUN-1996.
XX
PF   15-NOV-1994;   94JP-0280655.
XX
PR   15-NOV-1994;   94JP-0280655.
XX
PA   (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
XX
DR   WPI; 1996-316314/32.
DR   P-PSDB; AAR99141.
XX
PT   DNA encoding ligand-binding region contg. the CRH region of
PT   granulocyte-colony stimulating factor receptor  - useful in
PT   treatment of leukaemia resulting from proliferation of granulocytes
XX
PS   Claim 4; Page 12-14; 17pp; Japanese.
XX
CC   AAT35138 encodes a human protein of a ligand binding region of a G-CSF
CC   (granulocyte colony stimulating factor) receptor. The DNA and protein
CC   are used in the development and/or study of drugs which can be
CC   substituted for G-CSF. Such drugs are useful in the treatment of
CC   leukaemia resulting from granulocyte over-proliferation. The DNA may
CC   be expressed recombinantly to provide a high yield of the protein.
XX
SQ   Sequence 999 BP; 207 A; 347 C; 276 G; 169 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 17;  Length 999;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     966 GCTCCAGTCGCTCCA 952


RESULT   8
AAQ67887/c
ID   AAQ67887 standard; DNA; 1193 BP.
XX
AC   AAQ67887;
XX
DT   27-MAR-1995  (first entry)
XX
DE   Rat ciliary neutrophic factor-alpha DNA.
XX
KW   Ciliary neutrophic factor; neurological disease; haemorrhage; tumor;
KW   trauma; infection; Alzheimer's disease; Creuzfeld Jakob disease;
KW   Down's syndrome; central nervous system; ds.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             81..1058
FT                   /*tag=  a
XX
PN   WO9416721-A.
XX
PD   04-AUG-1994.
XX
PF   28-JAN-1994;   94WO-US01057.
XX
PR   29-JAN-1993;   93US-0010978.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Friedman B,  Ip NY,  Rudge J,  Wiegand S,  Yancopoulos GD;
XX
DR   WPI; 1994-263772/32.
DR   P-PSDB; AAR58304.
XX
PT   Promoting survival and proliferation of neurons to - with
PT   recombinant human ciliary neurotrophic factor, also new rat
PT   receptor for this factor, useful to treat neurological disorders
XX
PS   Claim 5; Fig.1; 49pp; English.
XX
CC   Survival and/or proliferation of corticospinal neurons or neurons in
CC   the subependymal zone in a patient are promoted by administration of
CC   recombinant ciliary neurtrophic factor.  The protein may be
CC   used to treat a wide range of neurological diseases, e.g haemorrhage,
CC   tumor, trauma, infection, Alzheimer's disease, Creuzfeld Jokob
CC   disease, Down's syndrome, etc.
XX
SQ   Sequence 1193 BP; 267 A; 382 C; 304 G; 240 T; 0 other;
```

```
RESULT   4
AAZ43552
ID   AAZ43552 standard; DNA; 22 BP.
XX
AC   AAZ43552;
XX
DT   21-FEB-2000  (first entry)
XX
DE   Human OB-R PCR primer 2.
XX
KW   OB-R; leptin; PCR primer; differentiation; bone marrow; osteopathic;
KW   stromal progenitor; osteoblastic lineage; treatment; osteoporosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9953939-A1.
XX
PD   28-OCT-1999.
XX
PF   20-APR-1999;   99WO-US08604.
XX
PR   20-APR-1998;   98US-0082320.
XX
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Burguera B,  Thomas T,  Riggs BL;
XX
DR   WPI; 2000-052683/04.
XX
PT   Inducing differentiation of bone marrow stromal progenitor cells to an
PT   osteoblastic lineage  -
XX
PS   Example 2; Page 17; 47pp; English.
XX
CC   This invention describes a novel method (A) of inducing differentiation
CC   of a bone marrow stromal progenitor cell to an osteoblastic lineage is
CC   new and comprises contacting the bone marrow stromal progenitor cell with
CC   an amount of leptin or its analog. The products of the invention have
CC   osteopathic activity. The method is useful for inducing differentiation
CC   of a bone marrow stromal progenitor cell to an osteoblastic lineage and
CC   for inducing bone formation in mammals. Therefore the method is useful
CC   for the treatment of osteoporosis and other conditions where bone
CC   formation is required. This sequence represents a PCR primer used in the
CC   amplification of human OB-R variants.
XX
SQ   Sequence 22 BP; 5 A; 9 C; 2 G; 6 T; 0 other;


  Query Match          92.0%;  Score 13.8;  DB 21;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db       2 actccagtcactcca 16


RESULT   5
AAT33516/c
ID   AAT33516 standard; cDNA to mRNA; 639 BP.
XX
AC   AAT33516;
XX
DT   24-OCT-1996  (first entry)
XX
DE   Human G-CSF receptor ligand binding region C-terminus coding sequence.
XX
KW   Granulocyte colony stimulating factor; G-CSF; C-terminus; mouse; human;
KW   ligand binding domain; E.coli; maltose binding protein; receptor;
KW   G-CSF-dependent disease; G-CSF abnormality; ss.
XX
OS   Homo sapiens.
XX
PN   JP08131172-A.
XX
PD   28-MAY-1996.
XX
PF   14-NOV-1994;   94JP-0278841.
XX
PR   14-NOV-1994;   94JP-0278841.
XX
PA   (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
XX
DR   WPI; 1996-303849/31.
DR   P-PSDB; AAW00648.
XX
PT   DNA coding for a ligand-binding region BC of G-CSF receptor  -
PT   useful for prevention or treatment of G-CSF diseases
XX
PS   Claim 2; Page 9-10; 11pp; Japanese.
XX
CC   This sequence represents the C-terminal domain of a ligand binding
CC   region of a human granulocyte colony stimulating factor (G-CSF) receptor.
CC    This sequence, the corresponding mouse sequence (see AAT33515), or a
CC   conserved fragment of both these sequences (see AAT33517) can be used in
CC   an expression vector for the production of the receptor.  The sequences
CC   can also be used in an expression vector containing E.coli maltose
CC   binding protein to produce a fusion protein.  The DNA can be used in the
CC   study of diseases related to the interaction between the G-CSF receptor
CC   and its ligand, as well as for the treatment or prevention of
CC   G-CSF-dependent diseases and abnormalities.  The recombinant
CC   ligand-binding region produced, is physiologically active and can be used
CC   in the study of the G-CSF receptor, such as analysis of its
CC   stereostructure.
XX
SQ   Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;


  Query Match          92.0%;  Score 13.8;  DB 17;  Length 639;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     606 GCTCCAGTCGCTCCA 592


RESULT   6
AAT68830/c
ID   AAT68830 standard; cDNA to mRNA; 990 BP.
XX
AC   AAT68830;
XX
DT   04-FEB-1998  (first entry)
XX
DE   cDNA for rheumatoid arthritis auto-antigen clone A.
XX
KW   Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
KW   prediction; synovial cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
XX
PN   WO9717441-A1.
XX
PD   15-MAY-1997.
XX
PF   06-NOV-1996;   96WO-JP03250.
XX
PR   07-NOV-1995;   95JP-0288957.
XX
```

PS Claim 12; Page 51; 87pp; English.
XX
CC 5 Degenerate hybridisation probes (AAT17870-74) are based on a
CC conserved motif (AAR92812) found in haemopoietin receptors. The
CC probes are used in the identification and/or cloning of genes
CC coding for novel haemopoietin receptors, e.g. the murine
CC interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such
CC receptors are defined by their ability to hybridise to the
CC probes under medium stringency conditions.
XX
SQ Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
||||||||||||||||
Db 1 rctccartcrctcca 15

RESULT 2
AAT64433
ID AAT64433 standard; DNA; 15 BP.
XX
AC AAT64433;
XX
DT 30-OCT-1997 (first entry)
XX
DE Haemopoietin receptor NR2 hybridising oligonucleotide HYB2.
XX
KW Haemopoietin receptor; new receptor 2; NR2; leptin; human;
KW autoimmune disease; nervous system; cerebral palsy;
KW trauma induced paralysis; vascular ischaemia; stroke;
KW neuronal tumour; motor neurone disease; Parkinson's disease;
KW Huntington's disease; Alzheimer's disease; multiple sclerosis;
KW peripheral neuropathy; heavy metal; alcohol; toxicity;
KW kidneyl failure; infectious disease; herpes; rubella; measles;
KW chicken pox; HIV; HTLV-1; therapy; probe; ss.
XX
OS Synthetic.
XX
PN WO9712037-A1.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-AU00607.
XX
PR 26-SEP-1995; 95AU-0005641.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Alexander WS, Gainsford T, Hilton DJ, Metcalf D;
PI Ng A, Nicola NA, Willsont;
XX
DR WPI; 1997-212896/19.
XX
PT Human haemopoietin receptor NR2, and corresponding DNA - used e.g.
PT for treatment of autoimmune diseases
XX
PS Claim 1; Page 68; 96pp; English.
XX
CC Oligonucleotide HYB2 hybridises under medium stringent conditions
CC to a novel DNA (see AAT64442) encoding human haemopoietin receptor
CC NR2 (AAW14841). It was used in the isolation of a partial NR2
CC sequence from a cDNA library constructed from the bone marrow
CC mRNA of a patient recovering from chemotherapy. NR2 and genetic
CC sequences encoding it can be used in the development of
CC (ant)agonists, therapeutics and diagnostic reagents based on
CC ligand interaction with the receptor.
XX
SQ Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
||||||||||||||||
Db 1 rctccartcrctcca 15

RESULT 3
AAV27138
ID AAV27138 standard; DNA; 15 BP.
XX
AC AAV27138;
XX
DT 29-SEP-1998 (first entry)
XX
DE Novel haemopoietin receptor probe 1.
XX
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW probe.
XX
OS Synthetic.
OS Mammalian.
XX
PN WO9811225-A2.
XX
PD 19-MAR-1998.
XX
PF 11-SEP-1997; 97WO-GB02479.
XX
PR 11-SEP-1996; 96AU-0002246.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
XX
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y;
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T;
PI Zhang J;
XX
DR WPI; 1998-260970/23.
XX
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
XX
PS Claim 3; Page 132; 182pp; English.
XX
CC The probes AAV27138 and AAV27139 are used to identify nucleic acid
CC molecules encoding a novel haemopoietin receptor (HR). Interaction
CC between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and it's
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
XX
SQ Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
||||||||||||||||
Db 1 rctccartcrctcca 15

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:40 ; Search time 301.32 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	92.0	15	17	AAT17871	Haemopoietin recep
	2	13.8	92.0	15	18	AAT64433	Haemopoietin recep
	3	13.8	92.0	15	19	AAV27138	Novel haemopoietin
	4	13.8	92.0	22	21	AAZ43552	Human OB-R PCR pri
c	5	13.8	92.0	639	17	AAT33516	Human G-CSF recept
c	6	13.8	92.0	990	18	AAT68830	cDNA for rheumatoi
c	7	13.8	92.0	999	17	AAT35138	DNA encoding cytok
c	8	13.8	92.0	1193	15	AAQ67887	Rat ciliary neutro
c	9	13.8	92.0	1383	18	AAT66164	Mouse interleukin-
	10	13.8	92.0	1419	21	AAC76452	Human ORFX ORF2007
c	11	13.8	92.0	1591	13	AAQ20195	Ciliary neurotroph
c	12	13.8	92.0	1591	14	AAQ39626	Sequence encoding
c	13	13.8	92.0	1591	16	AAQ83223	Human recombinant
c	14	13.8	92.0	1977	17	AAT14602	Human gp130 splice
	15	13.8	92.0	2096	19	AAV69318	M. fortuitum plasm
c	16	13.8	92.0	2119	22	AAC92350	Human haemopoietin
c	17	13.8	92.0	2369	17	AAQ74081	gp130 N-terminal f
c	18	13.8	92.0	2440	22	AAC92338	Human haemopoietin
c	19	13.8	92.0	2461	18	AAT75707	Murine leptin rece
c	20	13.8	92.0	2497	15	AAQ55941	Murine leukaemia i
c	21	13.8	92.0	2498	13	AAQ25800	mLIF-R. Mus muscu
c	22	13.8	92.0	2498	15	AAQ58426	Mouse LIF-R clone
c	23	13.8	92.0	2498	16	AAQ92271	Murine leukaemia i
c	24	13.8	92.0	2507	18	AAT98534	Natural splice var
c	25	13.8	92.0	2529	12	AAQ13857	Human GCSF recepto
c	26	13.8	92.0	2529	18	AAT75703	Murine leptin rece
c	27	13.8	92.0	2546	12	AAQ11579	Encodes granulocyt
c	28	13.8	92.0	2546	18	AAT47099	Human granulocyte
c	29	13.8	92.0	2562	16	AAQ95481	G-CSFR cDNA clone
c	30	13.8	92.0	2624	18	AAT98532	Coding sequence fo
c	31	13.8	92.0	2685	18	AAT97149	Ob protein recepto
c	32	13.8	92.0	2685	18	AAT97156	Ob protein recepto
c	33	13.8	92.0	2703	18	AAT75706	Murine leptin rece
c	34	13.8	92.0	2754	17	AAT14603	Human gp130 native
c	35	13.8	92.0	2868	18	AAT85578	Murine WSX recepto
c	36	13.8	92.0	2877	17	AAT12913	Haematopoietin rec
c	37	13.8	92.0	2877	18	AAT95781	Human OB-R variant
c	38	13.8	92.0	2880	17	AAT12912	Haematopoietin rec
c	39	13.8	92.0	2880	18	AAT95780	Human OB-R variant
c	40	13.8	92.0	2880	18	AAT74022	Variant form of hu
c	41	13.8	92.0	2931	12	AAQ11580	Clone 25-1 encodes
c	42	13.8	92.0	2933	18	AAT47100	Human granulocyte
c	43	13.8	92.0	2942	12	AAQ13856	Human GCSF recepto
c	44	13.8	92.0	2943	21	AAA62841	Human granulocyte
c	45	13.8	92.0	2948	18	AAT98533	Coding sequence fo

ALIGNMENTS

RESULT 1
AAT17871
ID AAT17871 standard; DNA; 15 BP.
XX
AC AAT17871;
XX
DT 21-MAY-1996 (first entry)
XX
DE Haemopoietin receptor probe HYB2.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN WO9607737-A1.
XX
PD 14-MAR-1996.
XX
PF 05-SEP-1995; 95WO-AU00578.
XX
PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ;
XX
DR WPI; 1996-171612/17.
XX
PT Nucleic acid encoding haemopoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists
XX

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                    /sex="hermaphrodite, male"
                    /tissue_type="whole animal"
                    /dev_stage="varied"
BASE COUNT      129 a     69 c     74 g     86 t      2 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 156;  Length 360;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    161 GCTCCAGTCGCTCCA 175


RESULT  15
FR0028454/c
LOCUS       FR0028454     360 bp    DNA             GSS       25-JUN-1998
DEFINITION  Fugu rubripes GSS sequence, clone 006I18bD2, genomic survey
            sequence.
ACCESSION   AL024826
VERSION     AL024826.1  GI:3262169
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
            Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
            biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .360
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 006I18"
                     /clone="006I18bD2"
BASE COUNT       87 a     85 c     91 g     92 t      5 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 222;  Length 360;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    169 GCTCCAGTCGCTCCA 155


Search completed: August 29, 2001, 19:22:13
Job time: 24136 sec
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  ORGANISM  Caenorhabditis briggsae
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 352)
  AUTHORS   Hillier,L., Chiapelli,B., Chissoe,S., Clark,N., Couch,J., Dubuque
            ,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le
            ,M., Mardis,E., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan
            ,F., Trevaskis,E., Waterston,R., Wohldmann,P. and Wilson,R.
  TITLE     Washington University Caenorhabditis briggsae EST project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Marra MA
            Washington University Genome Sequencing Center
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1455
            Fax: 314 286 1810
            Email: mmarra@watson.wustl.edu
            PCR_F: TGTAAAACGACGGCCAGTGAGCAAGTTCAGCCTGG
            PCR_B: CAGGAAACAGCTATGACCCTTATGAGTATTTCTTCCAGGGTA
            Source: Washington University Genome Sequencing Center
            PCR amplified DNA is available from Washington University Genome
            Sequencing Center. Aliquots of the library may be requested from P.
            Kuwabara (pek@mrc-lmb.cam.ac.uk).
            Seq primer: Commercially available M13 reverse dye primer.
FEATURES              Location/Qualifiers
     source           1. .352
                      /organism="Caenorhabditis briggsae"
                      /strain="G16 Gujarat"
                      /db_xref="taxon:6238"
                      /clone_lib="Kuwabara Mixed stage C. briggsae"
                      /note="Vector: Lambda gt10; Site_1: EcoRI; Site_2: EcoRI;
                      Stage:mixed, Sex:hermaphrodite. Library construction:
                      First strand oligo(dT) primed.  Second strand was as per
                      Gubler/Hoffman.  Ligated to EcoRI adaptors.  Library is
                      non-directional. Library is non-normalized. Library
                      constructed by P.E. Kuwabara.  Additional details on
                      construction of the  library are described in P.E.
                      Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
                      sequence: GAATTC CGTTGCTGTCG"
BASE COUNT       94 a     52 c    119 g     84 t      3 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 187;  Length 352;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     317 ACTCCAATCACTCCA 303


RESULT  13
AA272591/c
LOCUS       AA272591       355 bp    mRNA            EST       26-MAR-1997
DEFINITION  va75c12.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:737206 5'
            similar to gb:D17444 Mouse mRNA for soluble D-factor/LIF receptor,
            complete (MOUSE);, mRNA sequence.
ACCESSION   AA272591
VERSION     AA272591.1  GI:1910922
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R..
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:454254
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 209.
FEATURES              Location/Qualifiers
     source           1. .355
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:737206"
                      /clone_lib="Soares mouse NML"
                      /tissue_type="Liver"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATCTTTTTTTTTTTTTTTTT 3']
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      constructed and normalized by Bento Soares and M.Fatima
                      Bonaldo."
BASE COUNT       96 a     89 c     76 g     94 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 4;  Length 355;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     104 GCTCCAGTCACTCCA 90


RESULT  14
C65854
LOCUS       C65854         360 bp    mRNA            EST       22-SEP-1997
DEFINITION  C65854 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
            clone yk395h5 5', mRNA sequence.
ACCESSION   C65854
VERSION     C65854.1  GI:2424559
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            ,M., Miyata,A. and Nishigaki,A.
  TITLE     Expression map of the C.elegans genome
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Yuji Kohara
            Gene Library Lab
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .360
                      /organism="Caenorhabditis elegans"
                      /strain="CB1489 him-8(e1489)"
                      /db_xref="taxon:6239"
                      /clone="yk395h5"
                      /clone_lib="Yuji Kohara unpublished cDNA"
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```
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV1-BT0631-280
            200-084-f01_1&t3=2000-02-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 321.
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT0631"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       89 a     60 c    111 g     61 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 163;  Length 321;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    296 GCTCCAATCACTCCA 282


RESULT  11
BB209387/c
LOCUS       BB209387       331 bp    mRNA            EST       30-JUN-2000
DEFINITION  BB209387 RIKEN full-length enriched, 0 day neonate thymus Mus
            musculus cDNA clone A430092F05 3', mRNA sequence.
ACCESSION   BB209387
VERSION     BB209387.1  GI:8874340
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 331)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .331
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="A430092F05"
                     /clone_lib="RIKEN full-length enriched, 0 day neonate
                     thymus"
                     /tissue_type="thymus"
                     /dev_stage="0 day neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT       69 a     84 c     84 g     94 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 128;  Length 331;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    164 GCTCCAATCACTCCA 150


RESULT  12
R04486/c
LOCUS       R04486         352 bp    mRNA            EST       31-MAR-1995
DEFINITION  pk24c12.r1 Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae
            cDNA similar to SP:B0280.5, mRNA sequence.
ACCESSION   R04486
VERSION     R04486.1  GI:754222
KEYWORDS    EST.
SOURCE      Caenorhabditis briggsae.
```

```
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR1-CT0355-160
            200-003-f04&t3=2000-02-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 281.
FEATURES             Location/Qualifiers
     source          1. .281
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0355"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       98 a     48 c     64 g     71 t
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 121;  Length 281;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db     70 ACTCCAGTCACTCCA 56


RESULT   9
BB599621/c
LOCUS       BB599621      295 bp    mRNA            EST       01-DEC-2000
DEFINITION  BB599621 RIKEN full-length enriched, 9 days embryo Mus musculus
            cDNA clone D030001N11 5', mRNA sequence.
ACCESSION   BB599621
VERSION     BB599621.1  GI:11508222
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 295)
  AUTHORS   Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.
            , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
            ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
            Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
            Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
            ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
            Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .295
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="D030001N11"
                     /clone_lib="RIKEN full-length enriched, 9 days embryo"
                     /dev_stage="9 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3']. cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT       77 a     41 c     86 g     91 t
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 161;  Length 295;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db     65 ACTCCAGTCACTCCA 51


RESULT  10
BE080913/c
LOCUS       BE080913      321 bp    mRNA            EST       12-JUN-2000
DEFINITION  QV1-BT0631-280200-084-f01_1 BT0631 Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BE080913
VERSION     BE080913.1  GI:8471203
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
```

```
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/seq/gethtml.pl?t1=IL&t2=IL-BT161-010.html
            &t3=080399&t4=1)
            Seq primer: puc 18 forward.
FEATURES              Location/Qualifiers
     source           1. .254
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="BT161"
                      /sex="female"
                      /dev_stage="Adult"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No. 196
                      ,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
BASE COUNT       34 a      79 c      85 g      54 t       2 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 103;  Length 254;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     218 GCTCCAGTCACTCCA 232


RESULT   7
BB258685/c
LOCUS       BB258685       279 bp    mRNA            EST       06-JUL-2000
DEFINITION  BB258685 RIKEN full-length enriched, 7 days neonate cerebellum Mus
            musculus cDNA clone A730085O06 3', mRNA sequence.
ACCESSION   BB258685
VERSION     BB258685.1  GI:8951518
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 279)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of.thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .279
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="A730085O06"
                      /clone_lib="RIKEN full-length enriched, 7 days neonate
                      cerebellum"
                      /tissue_type="cerebellum"
                      /dev_stage="7 days neonate"
                      /lab_host="DH10B"
                      /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                      prepared and sequenced in Mouse Genome Encyclopedia
                      Project of Genome Exploration Research Group in Riken
                      Genomic Sciences Center and Genome Science Laboratory in
                      RIKEN. Division of Experimental Animal Research in Riken
                      contributed to prepare mouse tissues. 1st strand cDNA was
                      primed with a primer [5'
                      GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                      prepared by using trehalose thermo-activated reverse
                      transcriptase and subsequently enriched for full-length by
                      cap-trapper. cDNA went through one round of normalization
                      to Rot = 20.0 and subtraction to Rot = 459.0. Second
                      strand cDNA was prepared with the primer adapter of
                      sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                      3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                      modified pBluescript KS(+) after bulk excision from Lambda
                      FLC I."
BASE COUNT       58 a      84 c      65 g      72 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 129;  Length 279;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db      57 ACTCCAGTCACTCCA 43


RESULT   8
AW859532/c
LOCUS       AW859532       281 bp    mRNA            EST       19-MAY-2000
DEFINITION  MR1-CT0355-160200-003-f04 CT0355 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW859532
VERSION     AW859532.1  GI:7955225
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 281)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
```

,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .232
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930578B11"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT 67 a 53 c 38 g 74 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 123; Length 232;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db     56 ACTCCAATCACTCCA 70
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RESULT 5
AW859572
LOCUS AW859572 242 bp mRNA EST 19-MAY-2000
DEFINITION MR1-CT0355-180200-006-c12 CT0355 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW859572
VERSION AW859572.1 GI:7955265
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 242)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-CT0355-180200-006-c12&t3=2000-02-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 242.

FEATURES Location/Qualifiers
source 1. .242
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0355"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 65 a 58 c 40 g 79 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 121; Length 242;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RCTCCARTCRCTCCA 15
          :|||||:||:|||||
Db    163 ACTCCAGTCACTCCA 177
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RESULT 6
AI907996
LOCUS AI907996 254 bp mRNA EST 30-MAR-2000
DEFINITION IL-BT161-080399-010 BT161 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI907996
VERSION AI907996.1 GI:6498676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 254)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922

Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .181
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A330054L14"
/clone_lib="RIKEN full-length enriched, adult male spinal cord"
/sex="male"
/tissue_type="spinal cord"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

BASE COUNT 50 a 56 c 29 g 46 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 127; Length 181;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
:|||||:||:|||||
Db 51 ACTCCAGTCACTCCA 65

RESULT 3
AT002416
LOCUS AT002416 199 bp mRNA EST 10-SEP-1999
DEFINITION AT002416 Entamoeba histolytica trophozoite Entamoeba histolytica cDNA clone En044, mRNA sequence.
ACCESSION AT002416
VERSION AT002416.1 GI:5865820
KEYWORDS EST.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 199)
AUTHORS Kim,T.O., Hong,Y.C., Yu,H.S., Hwang,M.Y., Yun,H.C., Kong,H.H. and Chung,D.I.
TITLE Entamoeba histolytica trophozoite EST
JOURNAL Unpublished (1999)
COMMENT Contact: Chung DI
Department of Parasitology
Kyungpook National University School of Medicine
Dong-in dong 101, Chung-gu, Taegu 700 - 422, Republic of Korea
Tel: 82-53-420-6958
Fax: 82-53-422-9330
Email: dichung@bh.kyungpook.ac.kr
Submitted through BRIC(Biological Research Information Center) of Korea
URL: http://bric.postech.ac.kr/.
FEATURES Location/Qualifiers
source 1. .199
/organism="Entamoeba histolytica"
/strain="YS-27"
/db_xref="taxon:5759"
/clone="En044"
/clone_lib="Entamoeba histolytica trophozoite"
/dev_stage="trophozoite"
/lab_host="XL1 blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 82 a 33 c 38 g 45 t 1 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 106; Length 199;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
:|||||:||:|||||
Db 12 GCTCCAGTCACTCCA 26

RESULT 4
BB018457
LOCUS BB018457 232 bp mRNA EST 22-JUN-2000
DEFINITION BB018457 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930578B11 3', mRNA sequence.
ACCESSION BB018457
VERSION BB018457.1 GI:8190064
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 232)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M. , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y. , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y. , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I. , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino ,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13.8	92.0	140	115	AW408083	AW408083 UI-HF-BM0
2	13.8	92.0	181	127	BB189498	BB189498 BB189498
3	13.8	92.0	199	106	AT002416	AT002416 AT002416
4	13.8	92.0	232	123	BB018457	BB018457 BB018457
5	13.8	92.0	242	121	AW859572	AW859572 MR1-CT035
6	13.8	92.0	254	103	AI907996	AI907996 IL-BT161-
c 7	13.8	92.0	279	129	BB258685	BB258685 BB258685
c 8	13.8	92.0	281	121	AW859532	AW859532 MR1-CT035
c 9	13.8	92.0	295	161	BB599621	BB599621 BB599621
c 10	13.8	92.0	321	163	BE080913	BE080913 QV1-BT063
c 11	13.8	92.0	331	128	BB209387	BB209387 BB209387
c 12	13.8	92.0	352	187	R04486	R04486 pk24c12.r1
c 13	13.8	92.0	355	4	AA272591	AA272591 va75c12.r
14	13.8	92.0	360	156	C65854	C65854 C65854 Yuji
c 15	13.8	92.0	360	222	FR0028454	AL024826 Fugu rubr
c 16	13.8	92.0	364	30	AV401050	AV401050 AV401050
17	13.8	92.0	368	32	AV698306	AV698306 AV698306
c 18	13.8	92.0	381	14	AA984710	AA984710 am90a11.s
19	13.8	92.0	387	116	AW489097	AW489097 UI-M-BH3-
20	13.8	92.0	398	169	BF760838	BF760838 RC4-CT010
c 21	13.8	92.0	408	10	AA663262	AA663262 ab80f07.s
22	13.8	92.0	408	223	AQ060441	AQ060441 CIT-HSP-2
23	13.8	92.0	417	31	AV523125	AV523125 AV523125
c 24	13.8	92.0	423	110	AV743168	AV743168 AV743168
25	13.8	92.0	424	159	N75185	N75185 yw33a04.r1
26	13.8	92.0	424	168	BF706981	BF706981 281663 MA
c 27	13.8	92.0	426	175	BG263754	BG263754 WHE2348_F
c 28	13.8	92.0	428	231	AQ663435	AQ663435 HS_2160_B
c 29	13.8	92.0	435	227	AQ332979	AQ332979 HS_5005_B
30	13.8	92.0	435	231	AQ667104	AQ667104 HS_2106_B
c 31	13.8	92.0	444	9	AA619632	AA619632 vl54d09.r
c 32	13.8	92.0	446	2	AA082811	AA082811 zn25a04.r
c 33	13.8	92.0	448	8	AA495324	AA495324 fa01c03.r
c 34	13.8	92.0	453	188	R73050	R73050 yj94f12.r1
c 35	13.8	92.0	455	114	AW279627	AW279627 fj42c06.x
c 36	13.8	92.0	455	188	T21895	T21895 3903 Lambda
c 37	13.8	92.0	456	239	AZ151949	AZ151949 SP_0006_B
38	13.8	92.0	458	170	BF820788	BF820788 MR1-RT004
c 39	13.8	92.0	459	223	AQ022781	AQ022781 HS_2180_A
40	13.8	92.0	462	231	AQ648347	AQ648347 RPCI93-Ec
c 41	13.8	92.0	463	18	AI311382	AI311382 qo88e12.x
c 42	13.8	92.0	467	169	BF776672	BF776672 287536 MA
43	13.8	92.0	471	106	AT005091	AT005091 AT005091
44	13.8	92.0	477	145	BF200134	BF200134 WHE2252_D
45	13.8	92.0	482	231	AQ668275	AQ668275 HS_2121_B

ALIGNMENTS

```
RESULT   1
AW408083
LOCUS       AW408083      140 bp    mRNA            EST       16-FEB-2000
DEFINITION  UI-HF-BM0-adu-d-10-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone
            IMAGE:3062850 5', mRNA sequence.
ACCESSION   AW408083
VERSION     AW408083.1  GI:6927140
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 140)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
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                     Constructed from size fractionated cytoplasmic mRNA
                     (2.5-3.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT       30 a      57 c      29 g      24 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 115;  Length 140;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCARTCRCTCCA 15
           :|||||:||:|||||
Db     102 ACTCCAGTCACTCCA 116


RESULT   2
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LOCUS       BB189498      181 bp    mRNA            EST       30-JUN-2000
DEFINITION  BB189498 RIKEN full-length enriched, adult male spinal cord Mus
            musculus cDNA clone A330054L14 3', mRNA sequence.
ACCESSION   BB189498
VERSION     BB189498.1  GI:8850069
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 181)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
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            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:10 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

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Perfect score: 15
Sequence: 1 RCTCCARTCRCTCCA 15

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Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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ORIGIN


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Db    212 GCTCCAGGCGCTCCA 198


RESULT  14
MMU272227/c
LOCUS       MMU272227     701 bp    mRNA            ROD       17-FEB-2000
DEFINITION  Mus musculus mRNA for beta-A2-crystallin (cryba2 gene).
ACCESSION   AJ272227
VERSION     AJ272227.1  GI:7007338
KEYWORDS    beta-A2-crystallin; CRYBA2 gene.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Graw,J.
  TITLE     Sequence analysis of bata-A2-, beta-A4- and beta-B3-crystallin cDNA
            completes the identification of the members of this gene family in
            the mouse
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 701)
  AUTHORS   Graw,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Graw J., Institute of Mammalian Genetics,
            GSF-National Research Center for Environment and Health,
            Ingolstaedter Landstr. 1, D-86764 Neuherberg, GERMANY
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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BASE COUNT      151 a    206 c    206 g    138 t
ORIGIN


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  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :|||||  ||:|||||
Db    309 GCTCCAGGCACTCCA 295


RESULT  15
AF081273/c
LOCUS       AF081273      704 bp    mRNA            MAM       03-MAR-1999
DEFINITION  Bos taurus interleukin-4 receptor alpha chain mRNA, partial cds.
ACCESSION   AF081273
VERSION     AF081273.1  GI:4322316
KEYWORDS    .
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Trigona,W.T. and Estes,D.M.
  TITLE     Cloning of bovine homolog to interleukin-4 receptor alpha chain
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 704)
  AUTHORS   Trigona,W.T. and Estes,D.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1998) Veterinary Pathobiology, University of
            Missouri-Columbia, 201 Connaway Hall, Columbia, MO 65211, USA
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Bos taurus"
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                     TLRSGASYSARVKAWAQSYNSSWSAWSPSTKWLNYYEDTWEQRLQLGVGISCVIVLAV
                     CVSCYISITKIKKEWW"
BASE COUNT      171 a    223 c    184 g    126 t
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :|||||  ||:|||||
Db    561 GCTCCACGCGCTCCA 547


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Job time: 17238 sec
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          This sequence comes from Fig. 5.
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BASE COUNT      192 a    164 c    154 g    159 t
ORIGIN


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Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db     585 ACTCCATGCACTCCA 571


RESULT  11
BOVBA2/c
LOCUS       BOVBA2        696 bp    mRNA            MAM       26-APR-1993
DEFINITION  Cow beta-A2 crystallin (beta-A2) mRNA, complete cds.
ACCESSION   M60329
VERSION     M60329.1  GI:162726
KEYWORDS    beta-A2-crystallin; crystallin.
SOURCE      Bos taurus cDNA to mRNA.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   van Rens,G.L.M., Driessen,H.P.C., Nalini,V., Slingsby,C., de
            Jong,W.W. and Bloemendal,H.
  TITLE     Isolation and characterization of cDNAs encoding beta-A2- and
            beta-A4-crystallins: Heterologous interactions in the predicted
            beta-A4-beta-B2 heterodimer
  JOURNAL   Gene 102, 179-188 (1991)
  MEDLINE   91340151
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ORIGIN
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Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db     291 GCTCCAGGCACTCCA 277


RESULT  12
AF166331/c
LOCUS       AF166331      700 bp    mRNA            PRI       22-JUL-1999
DEFINITION  Homo sapiens beta crystallin A2 (CRYBA2) mRNA, complete cds.
ACCESSION   AF166331
VERSION     AF166331.1  GI:5566395
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Wistow,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1999) Molecular Structure and Function, National
            Eye Institute, 6/331, National Institutes of Health, Bethesda, MD
            20892-2740, USA
FEATURES             Location/Qualifiers
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ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 89;  Length 700;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db     275 ACTCCAGGCGCTCCA 261


RESULT  13
A64741/c
LOCUS       A64741        701 bp    DNA             PAT       29-MAR-1999
DEFINITION  Sequence 1 from Patent WO9730164.
ACCESSION   A64741
VERSION     A64741.1  GI:4530777
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Haseloff,J.P. and Hodge,S.
  TITLE     IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
  JOURNAL   Patent: WO 9730164-A 1 21-AUG-1997;
            MEDICAL RES COUNCIL (GB)
COMMENT     Other publication AU 1801497 19970902.
FEATURES             Location/Qualifiers
```

```
            78026 Versailles, France
REFERENCE   2  (bases 1 to 600)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W06A041"
BASE COUNT      169 a    131 c    142 g    158 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 14;  Length 600;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      16 ACTCCAAGCACTCCA 30


RESULT   8
CNS01ACZ
LOCUS       CNS01ACZ      600 bp    mRNA            PLN       02-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL112779
VERSION     AL112779.1  GI:5827398
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 600)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W08C111"
BASE COUNT      167 a    132 c    143 g    158 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 14;  Length 600;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      19 ACTCCAAGCACTCCA 33


RESULT   9
CNS01BUX
LOCUS       CNS01BUX      607 bp    mRNA            PLN       02-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL114721
VERSION     AL114721.1  GI:5829340
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 607)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 607)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .607
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W30E111"
BASE COUNT      172 a    132 c    145 g    157 t      1 others
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 14;  Length 607;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      32 ACTCCAAGCACTCCA 46


RESULT  10
S78505/c
LOCUS       S78505        669 bp    mRNA            PRI       07-MAR-2001
DEFINITION  Homo sapiens prolactin receptor mRNA, partial cds.
ACCESSION   S78505
VERSION     S78505.1  GI:999114
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fuh,G. and Wells,J.A.
  TITLE     Prolactin receptor antagonists that inhibit the growth of breast
            cancer cell lines
  JOURNAL   J. Biol. Chem. 270 (22), 13133-13137 (1995)
  MEDLINE   95286597
  REMARK    GenBank staff at the National Library of Medicine created this
```

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          :||||| ||:|||||
Db    317 ACTCCATGCACTCCA 303


RESULT   4
AR102280/c
LOCUS       AR102280      357 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 3 from patent US 6083753.
ACCESSION   AR102280
VERSION     AR102280.1  GI:12813078
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 357)
  AUTHORS   Kelly,P.A. and Nagano,M.
  TITLE     Soluble human prolactin receptors
  JOURNAL   Patent: US 6083753-A 3 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .357
                     /organism="unknown"
BASE COUNT       99 a     90 c     76 g     92 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 9;  Length 357;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db     317 ACTCCATGCACTCCA 303


RESULT   5
CNS01B4F
LOCUS       CNS01B4F      540 bp    mRNA            PLN       02-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL113767
VERSION     AL113767.1  GI:5828386
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 540)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W24H011"
BASE COUNT      156 a    121 c    128 g    135 t
ORIGIN
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  Query Match             88.0%;  Score 13.2;  DB 14;  Length 540;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      19 ACTCCAAGCACTCCA 33


RESULT   6
CNS01D2D
LOCUS       CNS01D2D      540 bp    mRNA            PLN       03-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL116285
VERSION     AL116285.1  GI:5831501
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2  (bases 1 to 540)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library to be analyzed within the framework of this
            project was created using a Botrytis cinerea strain which was grown
            under conditions of nitrogen deprivation, which is the normal
            situation for B. cinerea during its development on its host plant.
            The library was produced in an oriented direction, in the pBSII
            vector.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Botryotinia fuckeliana"
                     /strain="T4"
                     /db_xref="taxon:40559"
                     /note="Genoscope sequence ID : W33E081"
BASE COUNT      152 a    120 c    133 g    135 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 14;  Length 540;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db       5 ACTCCAAGCACTCCA 19


RESULT   7
CNS018S2
LOCUS       CNS018S2      600 bp    mRNA            PLN       02-SEP-1999
DEFINITION  Botrytis cinerea strain T4 cDNA library under conditions of
            nitrogen deprivation.
ACCESSION   AL110729
VERSION     AL110729.1  GI:5825016
KEYWORDS    cDNA library; nitrogen deprivation.
SOURCE      Botryotinia fuckeliana.
  ORGANISM  Botryotinia fuckeliana
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
```

	9	13.2	88.0	607	14	CNS01BUX	AL114721 Botrytis
c	10	13.2	88.0	669	97	S78505	S78505 Homo sapien
c	11	13.2	88.0	696	7	BOVBA2	M60329 Cow beta-A2
c	12	13.2	88.0	700	89	AF166331	AF166331 Homo sapi
c	13	13.2	88.0	701	9	A64741	A64741 Sequence 1
c	14	13.2	88.0	701	94	MMU272227	AJ272227 Mus muscu
c	15	13.2	88.0	704	7	AF081273	AF081273 Bos tauru
c	16	13.2	88.0	714	10	AX100243	AX100243 Sequence
	17	13.2	88.0	739	9	A86031	A86031 Sequence 69
	18	13.2	88.0	739	10	E66049	E66049 Genome DNA
c	19	13.2	88.0	780	53	CNS01EU1	AL141002 Anopheles
c	20	13.2	88.0	912	91	BC006285	BC006285 Homo sapi
c	21	13.2	88.0	1050	9	AR101845	AR101845 Sequence
c	22	13.2	88.0	1050	9	AR102285	AR102285 Sequence
c	23	13.2	88.0	1091	53	CNS06QRO	AL411034 T7 end of
c	24	13.2	88.0	1140	9	AX010400	AX010400 Sequence
c	25	13.2	88.0	1297	89	AF166329	AF166329 Homo sapi
	26	13.2	88.0	1448	13	ATHPROKINA	L05561 Arabidopsis
c	27	13.2	88.0	1472	88	AF107834	AF107834 Homo sapi
c	28	13.2	88.0	1566	89	AF349939	AF349939 Homo sapi
	29	13.2	88.0	1679	6	DDU03413	U03413 Dictyosteli
c	30	13.2	88.0	1681	94	MMU14412	U14412 Mus musculu
c	31	13.2	88.0	1713	94	AF347936	AF347936 Rattus no
c	32	13.2	88.0	1719	94	MMETL	X74953 M.musculus
c	33	13.2	88.0	1726	94	AF131077	AF131077 Rattus no
c	34	13.2	88.0	1757	11	BPSFIFII	D26449 Bacteriopha
c	35	13.2	88.0	1778	94	AF097723	AF097723 Rattus no
c	36	13.2	88.0	1794	89	AF119386	AF119386 Homo sapi
	37	13.2	88.0	1833	95	RATCALAA	D10480 Rat gene fo
c	38	13.2	88.0	1860	9	AX006440	AX006440 Sequence
c	39	13.2	88.0	1884	94	MMETL2912	X94160 M.musculus
c	40	13.2	88.0	1975	94	MMU69491	U69491 Mus musculu
c	41	13.2	88.0	1985	94	MMIL11	X98519 M.musculus
c	42	13.2	88.0	2116	94	MMU72520	U72520 Mus musculu
c	43	13.2	88.0	2178	6	DROPOXNUP	M86927 Fruitfly po
c	44	13.2	88.0	2213	91	BC002681	BC002681 Homo sapi
c	45	13.2	88.0	2219	91	D89016	D89016 Homo sapien

ALIGNMENTS

```
RESULT   1
A64746
LOCUS       A64746         108 bp    DNA             PAT       29-MAR-1999
DEFINITION  Sequence 6 from Patent WO9730164.
ACCESSION   A64746
VERSION     A64746.1  GI:4530782
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 108)
  AUTHORS   Haseloff,J.P. and Hodge,S.
  TITLE     IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
  JOURNAL   Patent: WO 9730164-A 6 21-AUG-1997;
            MEDICAL RES COUNCIL (GB)
COMMENT     Other publication AU 1801497 19970902.
FEATURES             Location/Qualifiers
     source          1. .108
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       18 a      25 c      46 g      19 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 9;  Length 108;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      32 GCTCCAGGCGCTCCA 46
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```
RESULT   2
HSPLR07/c
LOCUS       HSPLR07        172 bp    DNA             PRI       25-MAY-1999
DEFINITION  Homo sapiens prolactin receptor gene, exon 7.
ACCESSION   AF091867
VERSION     AF091867.1  GI:4886763
KEYWORDS    .
SEGMENT     7 of 10
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 172)
  AUTHORS   Hu,Z.Z., Zhuang,L., Meng,J., Leondires,M. and Dufau,M.L.
  TITLE     The human prolactin receptor gene structure and alternative
            promoter utilization: the generic promoter hPIII and a novel human
            promoter hP(N)
  JOURNAL   J. Clin. Endocrinol. Metab. 84 (3), 1153-1156 (1999)
  MEDLINE   99182102
   PUBMED   10084611
REFERENCE   2  (bases 1 to 172)
  AUTHORS   Hu,Z.Z., Zhuang,L., Meng,J.P. and Dufau,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-1998) ERRB, NICHD, 9000 Rockville Pike, Bethesda,
            MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .172
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
     exon            16. .157
                     /number=7
BASE COUNT       44 a      43 c      39 g      46 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 93;  Length 172;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db     129 ACTCCATGCACTCCA 115
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```
RESULT   3
AR101840/c
LOCUS       AR101840       357 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 3 from patent US 6083714.
ACCESSION   AR101840
VERSION     AR101840.1  GI:12812638
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 357)
  AUTHORS   Kelly,P.A. and Nagano,M.
  TITLE     Soluble human prolactin receptors
  JOURNAL   Patent: US 6083714-A 3 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .357
                     /organism="unknown"
BASE COUNT       99 a      90 c      76 g      92 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 9;  Length 357;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:51:58 ; Search time 1774.1 Seconds
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Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13.2	88.0	108	9	A64746	A64746 Sequence 6
2	c	13.2	88.0	172	93	HSPLR07	AF091867 Homo sapi
3	c	13.2	88.0	357	9	AR101840	AR101840 Sequence
4	c	13.2	88.0	357	9	AR102280	AR102280 Sequence
5		13.2	88.0	540	14	CNS01B4F	AL113767 Botrytis
6		13.2	88.0	540	14	CNS01D2D	AL116285 Botrytis
7		13.2	88.0	600	14	CNS018S2	AL110729 Botrytis
8		13.2	88.0	600	14	CNS01ACZ	AL112779 Botrytis

PN US6083714-A.
XX
PD 04-JUL-2000.
XX
PF 26-FEB-1997; 97US-0806597.
XX
PR 29-FEB-1996; 96US-0012503.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Kelly PA, Nagano M;
XX
DR WPI; 2000-464339/40.
DR P-PSDB; AAY96916.
XX
PT New soluble prolactin receptors useful as human growth hormone binding
PT protein and in x-ray crystallographic analysis for developing molecular
PT models which define the tertiary structure of the hormone-binding
PT domains
XX
PS Disclosure; Column 25-28; 26pp; English.
XX
CC Soluble human prolactin receptor (hPRLR) isoforms have been isolated from
CC the human gastrointestinal tract. The isoforms have a deletion in the
CC extra- or intracellular domain and are thought to be generated by
CC alternative splicing, since four clones (A, B, C and E) precisely lack
CC one or two exons. Except for clone C, the deletion in all other clones
CC resulted in a frameshift and produced a stop codon before the
CC transmembrane domain. The soluble hPRLR may be used as a binding protein
CC for human prolactin and/or human growth hormone, which can be used in
CC diagnostics for the detection and measurement of the binding ligand or in
CC therapeutics for binding to human prolactin and/or human growth hormone
CC to retard or inhibit their hormone activities. They may also be used in
CC place of monoclonal antibodies to provide solution-based radioligand
CC receptor assays, in receptor sandwich or enzymatic assays, and in X-ray
CC crystallographic analysis to develop molecular models, which define the
CC tertiary structure of the hormone-binding domains, where such information
CC would provide insight into the structure of the actual contact between a
CC hormone and its receptor. This structural information would be useful in
CC the design of peptides which have prolactin or growth hormone-like
CC agonistic or antagonistic activity.
XX
SQ Sequence 357 BP; 99 A; 90 C; 76 G; 92 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 357;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
:||||| ||:||||
Db 317 ACTCCATGCACTCCA 303

RESULT 15
AAA49977/c
ID AAA49977 standard; cDNA; 357 BP.
XX
AC AAA49977;
XX
DT 10-OCT-2000 (first entry)
XX
DE DNA encoding soluble isoform of human prolactin receptor.
XX
KW Prolactin receptor; human; isoform; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..72
FT /*tag= a
FT mat_peptide 73..354
FT /*tag= b
XX
PN US6083753-A.
XX
PD 04-JUL-2000.
XX
PF 14-NOV-1997; 97US-0970428.
XX
PR 29-FEB-1996; 96US-0012503.
PR 26-FEB-1997; 97US-0806597.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Kelly PA, Nagano M;
XX
DR WPI; 2000-464346/40.
DR P-PSDB; AAY95524.
XX
PT New recombinant DNA having a segment encoding a signal peptide joined
PT translationally to a segment encoding a soluble human prolactin
PT receptor useful as a hormone growth hormone binding protein, and in
PT x-ray crystallographic analysis -
XX
PS Claim 8; Column 25-28; 27pp; English.
XX
CC The present sequence is that of DNA encoding a newly identified
CC soluble isoform of the human prolactin receptor (PRLR). The DNA
CC lacks exons 5 and 6 of the full-length receptor, resulting in a
CC frameshift that produces a stop codon before the transmembrane domain,
CC making the putative protein product (see AAY95524) a secreted form of
CC the receptor. 6 Isoforms (see AAA49976-82) of human PRLR were
CC identified in human colonic Caco-2 and human breast cancer T-47D
CC cells. Recombinant DNA molecules encoding the soluble PRLRs are
CC provided, as well as expression vectors and host cells. The soluble
CC PRLRs may be used as binding proteins for human prolactin and/or
CC human growth hormone, which can be useful in diagnostics for the
CC detection and measurement of the binding ligand, or in therapeutics
CC for binding to human prolactin and/or human growth hormone to retard
CC or inhibit their hormone activities. They may also be used in place
CC of monoclonal antibodies to provide solution-based radioligand
CC receptor assays, in receptor sandwich or enzymatic assays, and in
CC x-ray crystallographic analysis to develop molecular models that
CC define the tertiary structure of the hormone-binding domains, where
CC such information would provide insight into the structure of the
CC actual contact between a hormone and its receptor. This structural
CC information would be useful in the design of peptides that have
CC prolactin or growth hormone-like agonistic or antagonistic activity.
XX
SQ Sequence 357 BP; 99 A; 90 C; 76 G; 92 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 357;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
:||||| ||:||||
Db 317 ACTCCATGCACTCCA 303

Search completed: August 29, 2001, 20:16:43
Job time: 7424 sec

```
  Query Match            88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     15 ACTCCATGCACTCCA 1


RESULT  12
AAZ90895/c
ID   AAZ90895 standard; DNA; 15 BP.
XX
AC   AAZ90895;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #123.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 44; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match            88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     15 ACTCCATGCACTCCA 1


RESULT  13
AAX92243
ID   AAX92243 standard; DNA; 20 BP.
XX
AC   AAX92243;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW   vaccine; neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydia pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB01890.
XX
PR   04-NOV-1998;   98US-0107078.
PR   21-NOV-1997;   97FR-0014673.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae
XX
PS   Page 1496; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading
CC   frames and other nucleic acid sequences from the genome of
CC   Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC   disease such as pneumonia and bronchitis and is thought to be a
CC   contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC   otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC   by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC   AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC   containing C. pneumoniae nucleotides sequences can also be used as
CC   immunogenic compositions, especially where the vector directs the
CC   expression of a neutralising epitope of C. pneumoniae.
XX
SQ   Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;


  Query Match            88.0%;  Score 13.2;  DB 20;  Length 20;
  Best Local Similarity  80.0%;  Pred. No. 2.7e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db      6 gctccaagcactcca 20


RESULT  14
AAA53588/c
ID   AAA53588 standard; cDNA; 357 BP.
XX
AC   AAA53588;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Soluble human prolactin receptor clone B.
XX
KW   hPRLR; soluble; prolactin receptor; gastrointestinal; splice variant;
KW   binding protein; prolactin; growth hormone; agonist; antagonist; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..357
FT                   /*tag=  a
FT                   /product= hPRLR_clone_B
XX
```

```
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 42; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :|||||  ||:|||||
Db      15 ACTCCAGGCACTCCA 1


RESULT  10
AAZ90877/c
ID   AAZ90877 standard; DNA; 15 BP.
XX
AC   AAZ90877;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #105.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :|||||  ||:|||||
Db      15 ACTCCAGGCACTCCA 1


RESULT  11
AAZ90883/c
ID   AAZ90883 standard; DNA; 15 BP.
XX
AC   AAZ90883;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #111.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
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CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:||||||
Db      15 ACTCCATGCACTCCA 1


RESULT   7
AAZ90837/c
ID   AAZ90837 standard; DNA; 15 BP.
XX
AC   AAZ90837;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #65.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 41; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:||||||
Db      15 ACTCCATGCACTCCA 1


RESULT   8
AAZ90861/c
ID   AAZ90861 standard; DNA; 15 BP.
XX
AC   AAZ90861;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #89.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 42; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:||||||
Db      15 ACTCCATGCACTCCA 1


RESULT   9
AAZ90872/c
ID   AAZ90872 standard; DNA; 15 BP.
XX
AC   AAZ90872;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #100.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
```

```
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 39; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      15 ACTCCATGCACTCCA 1


RESULT   5
AAZ90832/c
ID   AAZ90832 standard; DNA; 15 BP.
XX
AC   AAZ90832;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #60.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      15 ACTCCAGGCACTCCA 1


RESULT   6
AAZ90836/c
ID   AAZ90836 standard; DNA; 15 BP.
XX
AC   AAZ90836;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #64.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
```

```
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 3 C; 7 G; 3 T; 0 other;


  Query Match            88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     15 GCTCCAGGCACTCCA 1


RESULT   2
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ID   AAZ59267 standard; DNA; 15 BP.
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AC   AAZ59267;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #10.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 38; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;


  Query Match            88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     15 ACTCCAGGCACTCCA 1


RESULT   3
AAZ59278/c
ID   AAZ59278 standard; DNA; 15 BP.
XX
AC   AAZ59278;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #21.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 38; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;


  Query Match            88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity  80.0%;  Pred. No. 2.6e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     15 ACTCCATGCACTCCA 1


RESULT   4
AAZ59282/c
ID   AAZ59282 standard; DNA; 15 BP.
XX
AC   AAZ59282;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #25.
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:42 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-8
Perfect score: 15
Sequence: 1 RCTCCANGCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.2	88.0	15	21	AAZ59263	Human NR8 gene pro
c 2	13.2	88.0	15	21	AAZ59267	Human NR8 gene pro
c 3	13.2	88.0	15	21	AAZ59278	Human NR8 gene pro
c 4	13.2	88.0	15	21	AAZ59282	Human NR8 gene pro
c 5	13.2	88.0	15	21	AAZ90832	Human NR8 gene pro
c 6	13.2	88.0	15	21	AAZ90836	Human NR8 gene pro
c 7	13.2	88.0	15	21	AAZ90837	Human NR8 gene pro
c 8	13.2	88.0	15	21	AAZ90861	Human NR8 gene pro
c 9	13.2	88.0	15	21	AAZ90872	Human NR8 gene pro
c 10	13.2	88.0	15	21	AAZ90877	Human NR8 gene pro
c 11	13.2	88.0	15	21	AAZ90883	Human NR8 gene pro
c 12	13.2	88.0	15	21	AAZ90895	Human NR8 gene pro
13	13.2	88.0	20	20	AAX92243	PCR primer used to
c 14	13.2	88.0	357	21	AAA53588	Soluble human prol
c 15	13.2	88.0	357	21	AAA49977	DNA encoding solub
c 16	13.2	88.0	555	20	AAV90098	EST clone CW1682.
c 17	13.2	88.0	701	18	AAT94500	GAL4 DNA binding d
c 18	13.2	88.0	714	22	AAC85557	cDNA encoding CDIF
c 19	13.2	88.0	825	12	AAQ11855	Glutamate receptor
c 20	13.2	88.0	1050	21	AAA53593	Soluble human prol
c 21	13.2	88.0	1050	21	AAA49980	DNA encoding novel
c 22	13.2	88.0	1134	21	AAZ98101	Human secreted pro
c 23	13.2	88.0	1140	21	AAZ40400	Murine soluble int
24	13.2	88.0	1448	22	AAF31051	Protein kinase cod
c 25	13.2	88.0	1705	17	AAT17868	Murine interleukin
c 26	13.2	88.0	1714	17	AAT32613	Murine Etl-2 gene.
c 27	13.2	88.0	1767	21	AAA40493	Human fetal kidney
c 28	13.2	88.0	1778	18	AAV02296	Human secreted pro
c 29	13.2	88.0	1851	19	AAV82779	Clone bu45_2 isola
c 30	13.2	88.0	1863	21	AAZ98034	Human secreted pro
c 31	13.2	88.0	1884	21	AAZ58313	Human peptidase NA
c 32	13.2	88.0	1899	13	AAQ24321	Mutant thermostabl
c 33	13.2	88.0	1923	21	AAZ98139	Human signal pepti
c 34	13.2	88.0	2043	13	AAQ24320	Mutant thermostabl
c 35	13.2	88.0	2172	19	AAV02996	Mammalian Ena (Men
c 36	13.2	88.0	2277	13	AAQ24013	Mutant thermostabl
c 37	13.2	88.0	2370	13	AAQ24012	Mutant thermostabl
c 38	13.2	88.0	2505	13	AAQ24011	Mutant thermostabl
c 39	13.2	88.0	2690	20	AAZ20208	Sugarbeet raffinos
c 40	13.2	88.0	2723	12	AAQ10550	Human prolactin re
c 41	13.2	88.0	2898	19	AAV02998	Mouse neural Mena+
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ALIGNMENTS

RESULT 1
AAZ59263/c
ID AAZ59263 standard; DNA; 15 BP.
XX
AC AAZ59263;
XX
DT 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #6.
XX
KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
OS Homo sapiens.
XX
PN WO9967290-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-JP03351.
XX
PR 24-JUN-1998; 98JP-0214720.
PR 19-OCT-1998; 98JP-0297409.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
DR WPI; 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders -
XX
PS Example 1; Page 38; 176pp; Japanese.

```
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
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Qy       1 RCTCCANGCRCTCCA 15
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Db      57 ACTCCAGGCGCTCCA 71


RESULT  15
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LOCUS       AV081754      177 bp    mRNA            EST       25-JUN-1999
DEFINITION  AV081754 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210421D01, mRNA sequence.
ACCESSION   AV081754
VERSION     AV081754.1  GI:5213202
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 177)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
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ORIGIN


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  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
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Db      58 ACTCCAGGCGCTCCA 72


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  Query Match             88.0%;  Score 13.2;  DB 109;  Length 171;
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Qy      1 RCTCCANGCRCTCCA 15
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Db     53 ACTCCAGGCGCTCCA 67


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DEFINITION  AV072886 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200007C09, mRNA sequence.
ACCESSION   AV072886
VERSION     AV072886.1  GI:5192714
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 173)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
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ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     55 ACTCCAGGCGCTCCA 69


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DEFINITION  AV072630 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200005H20, mRNA sequence.
ACCESSION   AV072630
VERSION     AV072630.1  GI:5192458
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 174)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
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ORIGIN


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  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     56 ACTCCAGGCGCTCCA 70


RESULT  14
AV072658
LOCUS       AV072658      175 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV072658 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200005J24, mRNA sequence.
ACCESSION   AV072658
VERSION     AV072658.1  GI:5192486
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 175)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
```

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                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       26 a     36 c     56 g     46 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 242;  Length 164;
  Best Local Similarity   80.0%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :|||||  ||:|||||
Db      62 ACTCCAGGCACTCCA 48


RESULT  10
AV073140
LOCUS       AV073140      166 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV073140 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200008O09, mRNA sequence.
ACCESSION   AV073140
VERSION     AV073140.1  GI:5192968
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 166)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .166
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2200008O09"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT       34 a     49 c     33 g     47 t      3 others
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 109;  Length 166;
  Best Local Similarity   80.0%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :|||||  ||:|||||
Db      18 ACTCCAGGCGCTCCA 32


RESULT  11
AV076989
LOCUS       AV076989      171 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV076989 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210021D15, mRNA sequence.
ACCESSION   AV076989
VERSION     AV076989.1  GI:5196817
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210021D15"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT       39 a     53 c     32 g     47 t
ORIGIN
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            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .162
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2200006M08"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT       34 a     50 c     30 g     48 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 109;  Length 162;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      44 ACTCCAGGCGCTCCA 58


RESULT   8
BE069562
LOCUS       BE069562      162 bp    mRNA            EST       09-JUN-2000
DEFINITION  RC2-BT0389-090300-012-f12 BT0389 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE069562
VERSION     BE069562.1  GI:8414212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 162)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC2-BT0389-090
            300-012-f12&t3=2000-03-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 44
            High quality sequence stop: 162.
FEATURES             Location/Qualifiers
     source          1. .162
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT0389"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       51 a     33 c     37 g     41 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 163;  Length 162;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :||||| ||:|||||
Db      71 GCTCCATGCACTCCA 85


RESULT   9
AZ376266/c
LOCUS       AZ376266      164 bp    DNA             GSS       02-OCT-2000
DEFINITION  1M0130J06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0130J06 F, DNA sequence.
ACCESSION   AZ376266
VERSION     AZ376266.1  GI:10489966
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 164)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0130  row: J  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 164.
FEATURES             Location/Qualifiers
     source          1. .164
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0130J06"
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  Query Match             88.0%;  Score 13.2;  DB 109;  Length 159;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     47 ACTCCAGGCGCTCCA 61


RESULT   5
AV074451
LOCUS       AV074451      160 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV074451 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210009E18, mRNA sequence.
ACCESSION   AV074451
VERSION     AV074451.1  GI:5194279
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 160)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .160
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210009E18"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT       35 a     49 c     29 g     47 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 109;  Length 160;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     42 ACTCCAGGCGCTCCA 56


RESULT   6
AV074715
LOCUS       AV074715      161 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV074715 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210010H07, mRNA sequence.
ACCESSION   AV074715
VERSION     AV074715.1  GI:5194543
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 161)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .161
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210010H07"
                     /clone_lib="Mus musculus stomach C57BL/6J adult"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT       36 a     42 c     32 g     49 t      2 others
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 109;  Length 161;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :||||| ||:|||||
Db     42 ACTCCAGGCGCTCCA 56


RESULT   7
AV072831
LOCUS       AV072831      162 bp    mRNA            EST       24-JUN-1999
DEFINITION  AV072831 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200006M08, mRNA sequence.
ACCESSION   AV072831
VERSION     AV072831.1  GI:5192659
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 162)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
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            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .135
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="2210413F10"
                      /clone_lib="Mus musculus stomach C57BL/6J adult"
                      /sex="male"
                      /tissue_type="stomach"
                      /dev_stage="adult"
BASE COUNT       26 a     41 c     26 g     42 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 109;  Length 135;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :|||||  ||:|||||
Db     16 ACTCCAGGCGCTCCA 30


RESULT   3
AV081442
LOCUS       AV081442      137 bp    mRNA            EST       25-JUN-1999
DEFINITION  AV081442 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210419B03, mRNA sequence.
ACCESSION   AV081442
VERSION     AV081442.1  GI:5212890
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
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BASE COUNT       29 a     41 c     27 g     40 t
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGCRCTCCA 15
          :|||||  ||:|||||
Db     20 ACTCCAGGCGCTCCA 34


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DEFINITION  AV072952 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2200007I01, mRNA sequence.
ACCESSION   AV072952
VERSION     AV072952.1  GI:5192780
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 159)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
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            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
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SUMMARIES

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3	13.2	88.0	137	109	AV081442	AV081442 AV081442
4	13.2	88.0	159	109	AV072952	AV072952 AV072952
5	13.2	88.0	160	109	AV074451	AV074451 AV074451
6	13.2	88.0	161	109	AV074715	AV074715 AV074715
7	13.2	88.0	162	109	AV072831	AV072831 AV072831
8	13.2	88.0	162	163	BE069562	BE069562 RC2-BT038
c 9	13.2	88.0	164	242	AZ376266	AZ376266 1M0130J06
10	13.2	88.0	166	109	AV073140	AV073140 AV073140
11	13.2	88.0	171	109	AV076989	AV076989 AV076989
12	13.2	88.0	173	109	AV072886	AV072886 AV072886
13	13.2	88.0	174	109	AV072630	AV072630 AV072630
14	13.2	88.0	175	109	AV072658	AV072658 AV072658
15	13.2	88.0	177	109	AV081754	AV081754 AV081754
16	13.2	88.0	179	109	AV058439	AV058439 AV058439
c 17	13.2	88.0	179	219	CNS00TGF	AL089661 Arabidops
18	13.2	88.0	180	109	AV077479	AV077479 AV077479
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22	13.2	88.0	192	109	AV077830	AV077830 AV077830
23	13.2	88.0	192	145	BF145876	BF145876 WHE1833_F
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25	13.2	88.0	194	109	AV072872	AV072872 AV072872
26	13.2	88.0	195	109	AV088929	AV088929 AV088929
27	13.2	88.0	200	109	AV072772	AV072772 AV072772
28	13.2	88.0	202	109	AV072097	AV072097 AV072097
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32	13.2	88.0	211	174	BG141411	BG141411 ia38g01.y
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35	13.2	88.0	224	109	AV072779	AV072779 AV072779
36	13.2	88.0	227	109	AV072787	AV072787 AV072787
37	13.2	88.0	229	109	AV072799	AV072799 AV072799
38	13.2	88.0	231	109	AV074114	AV074114 AV074114
39	13.2	88.0	234	109	AV072750	AV072750 AV072750
c 40	13.2	88.0	240	5	AA319785	AA319785 EST22073
41	13.2	88.0	240	107	AU071883	AU071883 AU071883
42	13.2	88.0	241	28	AV288598	AV288598 AV288598
c 43	13.2	88.0	243	22	AI618724	AI618724 zewp0296.
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ALIGNMENTS

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RESULT   1
BG607593
LOCUS       BG607593      119 bp    mRNA            EST       17-APR-2001
DEFINITION  WHE2480_H02_O04ZS Triticum monococcum early reproductive apex cDNA
            library Triticum monococcum cDNA clone WHE2480_H02_O04, mRNA
            sequence.
ACCESSION   BG607593
VERSION     BG607593.1  GI:13657576
KEYWORDS    EST.
SOURCE      Triticum monococcum.
  ORGANISM  Triticum monococcum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 119)
  AUTHORS   Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
            ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
            Stamova,B. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Early reproductive apex cDNA library from Triticum
            monococcum
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .119
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                     Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and
                     poly(A) RNA were prepared from apex at  double-ridge stage
                     to terminal-spikelet stage during transition from
                     vegetative state to flower state, a cDNA library was made,
                     and the  cDNA clones were in vivo excised at the
                     University of California, Davis  (V. Echenique, B. Stamova
                     , J. Dubcovsky).  Plasmid DNA preparations and  DNA
                     sequencing were performed in the OD Anderson lab (all
                     other authors)."
BASE COUNT       13 a     47 c     46 g     13 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 155;  Length 119;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGCRCTCCA 15
           :|||||  ||:|||||
Db      69 GCTCCATGCACTCCA 83


RESULT   2
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LOCUS       AV080202      135 bp    mRNA            EST       25-JUN-1999
DEFINITION  AV080202 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
            clone 2210413F10, mRNA sequence.
ACCESSION   AV080202
VERSION     AV080202.1  GI:5211650
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 135)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
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            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:13 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

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Perfect score: 15
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db     387 ACTCCATGGGCTCCA 401


RESULT  15
MMU276872/c
LOCUS       MMU276872     573 bp    mRNA            ROD       02-FEB-2001
DEFINITION  Mus musculus mRNA for GDNF family receptor alpha 4, putative
            secreted isoform (Gfra4 gene).
ACCESSION   AJ276872
VERSION     AJ276872.1  GI:7688070
KEYWORDS    alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
  TITLE     Expression and alternative splicing of mouse Gfra4 suggest roles in
            endocrine cell development
  JOURNAL   Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
  MEDLINE   20319126
REFERENCE   2  (bases 1 to 573)
  AUTHORS   Airaksinen,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
            Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
            9), 00014 University of Helsinki, FINLAND
FEATURES             Location/Qualifiers
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                     /translation="MAHCMESALLLLLLLGSASFTDGNRCVDAAEACTADERCQQLRS
                     EYVARCLGRAAPGGRPGPGGCVRSRCRRALRRFFARGPPALTHALLFCGCEGSACAER
                     RRQTFAPACAFSGPGLVPPSCLEPLERCERSRLCRCVRAGRAGPLTRVRARAGPVSLP
                     SRPHALPRPAPATAARRRGARVVCASTQAS"
BASE COUNT       49 a    213 c    215 g     96 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 94;  Length 573;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db     385 GCTCCAGGGGCTCCA 371


Search completed: August 29, 2001, 19:52:01
Job time: 17239 sec
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```
SOURCE      Echinometra mathaei.
  ORGANISM  Mitochondrion Echinometra mathaei
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
            Echinometra.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
  TITLE     Speciation and population genetic structure in tropical Pacific sea
            urchins
  JOURNAL   Evolution 51 (5), 1506-1517 (1997)
REFERENCE   2  (bases 1 to 450)
  AUTHORS   Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1997) OEB, Harvard University, 16 Divinity
            Avenue, Cambridge, MA 02138, USA
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Echinometra mathaei"
                     /organelle="mitochondrion"
                     /isolate="Nm4"
                     /db_xref="taxon:31178"
     CDS             <1. .>450
                     /codon_start=1
                     /transl_table=9
                     /product="cytochrome oxidase subunit I"
                     /protein_id="AAB69575.1"
                     /db_xref="GI:2353672"
                     /translation="HPEVYILILPGFGMISHVIAHYSGKREPFGYLGMVYAMIAIGVL
                     GVLVWAHHMFTVGMDVDTRAXXXAATMIIAVPTGIKVFSWMAXLQGSNLQWETPLFWA
                     LGFVFLFTLGGLTGIVLANSSIDVVLHDTYYVVAHFHYVXSMGAVFAI"
BASE COUNT      117 a    103 c     93 g    125 t     12 others
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 5;  Length 450;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db    137 ACTCCAAGGACTCCA 123


RESULT  13
G36845
LOCUS       G36845        477 bp    DNA             STS       31-DEC-1997
DEFINITION  SHGC-60507 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G36845
VERSION     G36845.1  GI:2734512
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Myers,R.M.
  TITLE     Human STSs (1997)
  JOURNAL   Unpublished (1997)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu
            Primer A: GCTGCCGACAGACAGTTTTG
            Primer B: ATGCAGCATGAAGCATGGAG
            STS size: 205
            PCR Profile:
                    Initial incubation: 95 degrees C for 10 minutes

                    Denaturation:       94 degrees C for 30 seconds
                    Annealing:          60 degrees C for 30 seconds
                    Polymerization:     72 degrees C for 23 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:                   25 ng
                    Primer:                     each 1 uM
                    dNTPs:                      each 200 uM
                    AmpliTaq Gold Polymerase:   0.07 units/ul
                    Total Vol:                  5 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50 mM
                    Tris-HCl:       10 mM
                    pH:             8.3

            BAC end sequences from L. Hood at University of Washington.
            Designed and developed at the Stanford Human Genome Center.
FEATURES             Location/Qualifiers
     source          1. .477
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="16"
                     /clone_lib="Human"
     STS             82. .286
     primer_bind     82. .101
     primer_bind     complement(267. .286)
BASE COUNT      113 a    131 c    112 g    121 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 54;  Length 477;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db    142 GCTCCAGGGACTCCA 156


RESULT  14
MMRARB3
LOCUS       MMRARB3       534 bp    mRNA            ROD       16-APR-1991
DEFINITION  Mouse RAR-beta mRNA for retinoic acid receptor-beta 3 isoform.
ACCESSION   X56574
VERSION     X56574.1  GI:53905
KEYWORDS    RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
            2 isoform.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Chambon,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-1990) Chambon P., LGME/CRNS- U184/INSERM -
            Institute de Chimie Biologique, 11 rue Humann, 67085
            STRASBOURG-Cedex, France
REFERENCE   2  (bases 1 to 534)
  AUTHORS   Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
            Ruffenach,F., Leroy,P. and Chambon,P.
  TITLE     Differentially expressed isoforms of the mouse retinoic acid
            receptor beta generated by usage of two promoters and alternative
            splicing
  JOURNAL   EMBO J. 10 (1), 71-81 (1991)
  MEDLINE   91114714
COMMENT     See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data
            kindly reviewed (18-FEB-1991) by Chambon P.
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
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          :|||||| ||:||||||
Db    121 ACTCCATGGACTCCA 107


RESULT   9
I49083/c
LOCUS       I49083         396 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 6 from patent US 5627264.
ACCESSION   I49083
VERSION     I49083.1  GI:2467546
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 396)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5627264-A 6 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .396
                     /organism="unknown"
BASE COUNT       98 a     96 c     95 g    107 t
ORIGIN


  Query Match           88.0%;  Score 13.2;  DB 10;  Length 396;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||| ||:||||||
Db    121 ACTCCATGGACTCCA 107


RESULT  10
SAICD59A/c
LOCUS       SAICD59A       396 bp    mRNA            PRI       14-MAR-1994
DEFINITION  Saimiri sciureus complement regulatory protein (CD59) mRNA,
            complete cds.
ACCESSION   L22859
VERSION     L22859.1  GI:404796
KEYWORDS    complement regulatory protein.
SOURCE      Saimiri sciureus.
  ORGANISM  Saimiri sciureus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
            Saimiri.
REFERENCE   1  (bases 1 to 396)
  AUTHORS   Rother,R.P., Rollins,S.A., Fodor,W.L., Albrecht,J.C., Setter,E.,
            Fleckenstein,B. and Squinto,S.P.
  TITLE     Inhibition of complement-mediated cytolysis by the terminal
            complement inhibitor of herpesvirus saimiri
  JOURNAL   J. Virol. 68 (2), 730-737 (1994)
  MEDLINE   94118421
FEATURES             Location/Qualifiers
     source          1. .396
                     /organism="Saimiri sciureus"
                     /db_xref="taxon:9521"
                     /cell_line="DPSO 114/74"
                     /tissue_type="lung"
                     /tissue_lib="ATCC CCL194"
     gene            1. .396
                     /gene="CD59"
     CDS             1. .396
                     /gene="CD59"
                     /note="homologue of human CD59"
                     /codon_start=1
                     /product="complement regulatory protein"
                     /protein_id="AAA16747.1"
                     /db_xref="GI:404797"
                     /translation="MGIQGGSVLFGLLLVLAVFCHSGNSLQCYSCPLPTMESMECTAS
                     TNCTSNLDSCLIAKAGSGVYYRCWKFDDCSFKRISNQLSETQLKYHCCKKNLCNVKEV
                     LENGGTTLSKKTILLLVTPFLAAAWSRHP"
BASE COUNT       98 a     96 c     95 g    107 t
ORIGIN


  Query Match           88.0%;  Score 13.2;  DB 97;  Length 396;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||| ||:||||||
Db    121 ACTCCATGGACTCCA 107


RESULT  11
AF221064
LOCUS       AF221064       413 bp    mRNA            ROD       07-MAR-2000
DEFINITION  Meriones unguiculatus calcium-sensing receptor (CaSR) mRNA, partial
            cds.
ACCESSION   AF221064
VERSION     AF221064.1  GI:7188643
KEYWORDS    .
SOURCE      Mongolian gerbil.
  ORGANISM  Meriones unguiculatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
            Meriones.
REFERENCE   1  (bases 1 to 413)
  AUTHORS   Wonneberger,K., Scofield,M.A. and Wangemann,P.
  TITLE     Evidence for a calcium sensing receptor in the vascular smooth
            muscle cells of the spiral modiolar artery
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 413)
  AUTHORS   Wangemann,P. and Scofield,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2000) Pharmacology, Creighton University, 2500
            California Plaza, Omaha, NE 68178, USA
FEATURES             Location/Qualifiers
     source          1. .413
                     /organism="Meriones unguiculatus"
                     /db_xref="taxon:10047"
                     /tissue_type="spiral modiolar artery; kidney"
     gene            <1. .>413
                     /gene="CaSR"
     CDS             <1. .>413
                     /gene="CaSR"
                     /codon_start=3
                     /product="calcium-sensing receptor"
                     /protein_id="AAF37826.1"
                     /db_xref="GI:7188644"
                     /translation="AFKSRKLPENFNEAKFITFSMLIFFIVWISFIPAYASTYGKFVS
                     AVEVIAILAASFGLLACIFFNKVYIILFKPSRNTIEEVRCSTAAHAFKVAARATLRRS
                     NVSRKRSSSLGGSTGSIPSSSMSSKSNSEDPFPQP"
BASE COUNT       79 a    149 c    103 g     82 t
ORIGIN


  Query Match           88.0%;  Score 13.2;  DB 94;  Length 413;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||| ||:||||||
Db    343 GCTCCACGGGCTCCA 357


RESULT  12
AF018838/c
LOCUS       AF018838       450 bp    DNA             INV       05-MAR-2001
DEFINITION  Echinometra mathaei isolate Nm4 cytochrome oxidase subunit I gene,
            partial cds; mitochondrial gene for mitochondrial product.
ACCESSION   AF018838
VERSION     AF018838.1  GI:2353671
KEYWORDS    .
```

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          date_of_search = 15-12-1995.
FEATURES             Location/Qualifiers
     source          1. .325
                     /organism="Drosophila melanogaster"
                     /strain="Oregon-R"
                     /db_xref="taxon:7227"
                     /clone="128B5"
BASE COUNT       82 a     76 c     75 g     92 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 54;  Length 325;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    121 ACTCCATGGGCTCCA 135


RESULT   6
MMRARB1
LOCUS       MMRARB1       360 bp    mRNA            ROD       16-APR-1991
DEFINITION  Mouse RAR-beta mRNA for retinoic acid receptor-beta 1 isoform.
ACCESSION   X56569
VERSION     X56569.1  GI:53901
KEYWORDS    RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
            1 isoform.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Chambon,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-1990) Chambon P., LGME/CRNS- U184/INSERM -
            Institute de Chimie Biologique, 11 rue Humann, 67085
            STRASBOURG-Cedex, France
REFERENCE   2  (bases 1 to 360)
  AUTHORS   Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
            Ruffenach,F., Leroy,P. and Chambon,P.
  TITLE     Differentially expressed isoforms of the mouse retinoic acid
            receptor beta generated by usage of two promoters and alternative
            splicing
  JOURNAL   EMBO J. 10 (1), 71-81 (1991)
  MEDLINE   91114714
COMMENT     See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data
            kindly reviewed (18-FEB-1991) by Chambon P.
FEATURES             Location/Qualifiers
     source          1. .360
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="14A"
                     /cell_line="F9, P19"
     mRNA            1. .360
                     /gene="RAR-beta"
     gene            1. .360
                     /gene="RAR-beta"
     exon            1. .316
                     /gene="RAR-beta"
                     /note="exon 1"
     mat_peptide     139. .>360
                     /gene="RAR-beta"
                     /product="retinoic acid receptor- beta 1 isoform"
     CDS             139. .>360
                     /gene="RAR-beta"
                     /codon_start=1
                     /product="retinoic acid receptor- beta 1 isoform"
                     /protein_id="CAA39918.1"
                     /db_xref="GI:53902"
                     /db_xref="MGD:MGI:97857"
                     /db_xref="SWISS-PROT:P22605"
                     /translation="MSTSSHACPVPAVRGHMTHYPAAPYPLLFPPVIRGLSLPPLHGL
                     HGHPPPSGCSTPSPATIETQSTSSEELVPS"
     exon            317. .>360
                     /gene="RAR-beta"
                     /note="exon 4"
BASE COUNT       74 a    125 c     80 g     81 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 94;  Length 360;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    258 ACTCCATGGGCTCCA 272


RESULT   7
AR064381/c
LOCUS       AR064381      396 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 3 from patent US 5847082.
ACCESSION   AR064381
VERSION     AR064381.1  GI:5993689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 396)
  AUTHORS   Rother,R., Rollins,S. and Squinto,S.P.
  TITLE     Terminal complement inhibitor fusion proteins
  JOURNAL   Patent: US 5847082-A 3 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .396
                     /organism="unknown"
BASE COUNT       98 a     96 c     95 g    107 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 9;  Length 396;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    121 ACTCCATGGACTCCA 107


RESULT   8
I41335/c
LOCUS       I41335        396 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 6 from patent US 5624837.
ACCESSION   I41335
VERSION     I41335.1  GI:2081925
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 396)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Nucleic acid encoding chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5624837-A 6 29-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .396
                     /organism="unknown"
BASE COUNT       98 a     96 c     95 g    107 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 10;  Length 396;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
```

```
           9 Cambridge Center, Cambridge MA 02142 USA
           Tel: 617 252 1900
           Fax: 617 252 1902
           Email: thudson@genome.wi.mit.edu

           Primer A: AAAACAAAAACAGCGCATGA
           Primer B: CCTTGACCCACCTTGAGAGA
           STS size: 277
           PCR Profile:
                 Presoak:
                 Denaturation:
                 Annealing: 56 degrees C
                 Polymerization:
                 PCR Cycles: 35
                 Thermal Cycler:
           Protocol:
               Template: 10 ng
               Primer: each 5 pM
               dNTPs: each 4 nM
               Taq Polymerase: 0.025 units/ul
               Total Vol: 20 ul

           Buffer:
               MgCl2: 1.5 mM
               KCl: 50 mM
               Tris-HCL: 10 mM
               pH: 9.3

           Prepared with primer pairs derived from Z38906 -- dbEST.
FEATURES             Location/Qualifiers
     source          1. .310
                     /organism="Homo sapiens"
     STS             33. .309
     primer_bind     33. .52
     primer_bind     complement(290. .309)
BASE COUNT       89 a     90 c     50 g     81 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 54;  Length 310;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    211 ACTCCAGGGGCTCCA 225


RESULT   4
E11372/c
ID   E11372     standard; RNA; ROD; 324 BP.
XX
AC   E11372;
XX
SV   E11372.1
XX
DT   07-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   cDNA encoding mouse ligand-binding region protein(BC) of G-CSF receptor.
XX
KW   JP 1996131172-A/3.
XX
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX
RN   [1]
RP   1-324
RA   Ota Y., Anaguchi H.;
RT   "DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
RT   STIMULATING FACTOR RECEPTOR";
RL   Patent number JP1996131172-A/3, 28-MAY-1996.
RL   TANPAKU KOGAKU KENKYUSHO:KK.
XX
CC   OS   Mus sp. (mouse)
CC   PN   JP 1996131172-A/3
CC   PD   28-MAY-1996
CC   PF   14-NOV-1994 JP 1994278841
CC   PI   OTA YOSHIMI, ANAGUCHI HIROYUKI
CC   PC   C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
CC   PC   C12R1:19),
CC   PC   (C12P21/02,C12R1:19);
CC   CC   strandedness: Double;
CC   CC   topology: Linear;
CC   CC   hypothetical: No;
CC   CC   anti-sense: No;
CC   FH   Key             Location/Qualifiers
CC   FH
CC   FT   source          1. .324
CC   FT                   /organism="Mus sp."
CC   FT                   /clone="pMALP-mBC"
CC   FT   mat_peptide     1. .324
CC   FT                   /product="mouse ligand-binding region
CC   FT                   protein(BC) of G-CSF
CC   FT                   receptor"
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .324
FT                   /db_xref="taxon:10095"
FT                   /organism="Mus sp."
XX
SQ   Sequence 324 BP; 63 A; 103 C; 89 G; 69 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 45;  Length 324;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    294 GCTCCAGGGGCTCCA 280


RESULT   5
DM128B5S
LOCUS       DM128B5S      325 bp    DNA             STS       16-APR-1996
DEFINITION  D. melanogaster STS determined from European Mapping Project
            cosmid, sequence tagged site.
ACCESSION   Z71056
VERSION     Z71056.1  GI:1263558
KEYWORDS    STS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 325)
  AUTHORS   European Drosophila Mapping,Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
            Downing St., Cambridge CB2 3EH, England
COMMENT     STS_name = Dm128B5S
            clone_name = 128B5
            STS_from_promoter = SP6
            vector_class = cosmid, Lorist 6
            origin_of_clone = Oregon-R
            in_situ_site_primary = 54F
            BLAST_program = BLASTN
            database_searched = EMBL
            database_version = 45.0 and updates till date_of_search
            date_of_search = 08-01-1996
            BLAST_program = BLASTX
            database_searched = SWISSPROT
            database_version = 32.0
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c	9	13.2	88.0	396	10	I49083 I49083 Sequence 6
c	10	13.2	88.0	396	97	SAICD59A L22859 Saimiri sci
	11	13.2	88.0	413	94	AF221064 AF221064 Meriones
c	12	13.2	88.0	450	5	AF018838 AF018838 Echinomet
	13	13.2	88.0	477	54	G36845 G36845 SHGC-60507
	14	13.2	88.0	534	94	MMRARB3 X56574 Mouse RAR-b
c	15	13.2	88.0	573	94	MMU276872 AJ276872 Mus muscu
c	16	13.2	88.0	600	94	MMU276515 AJ276515 Mus muscu
c	17	13.2	88.0	639	45	E09856 E09856 cDNA encodi
c	18	13.2	88.0	639	45	E11370 E11370 cDNA encodi
	19	13.2	88.0	678	13	AF305546 AF305546 Aspergill
	20	13.2	88.0	700	72	AC057116 AC057116 Giardia i
c	21	13.2	88.0	765	45	E11423 E11423 DNA encodin
c	22	13.2	88.0	779	3	MXAORFAA M79325 Myxococcus
c	23	13.2	88.0	783	10	AX090395 AX090395 Sequence
c	24	13.2	88.0	783	94	MMU276870 AJ276870 Mus muscu
c	25	13.2	88.0	792	10	AX068319 AX068319 Sequence
c	26	13.2	88.0	795	10	AX090391 AX090391 Sequence
	27	13.2	88.0	802	95	S70577 S70577 RAR beta 1/
c	28	13.2	88.0	810	94	MMU276514 AJ276514 Mus muscu
	29	13.2	88.0	819	91	CJU52115 U52115 Callithrix
c	30	13.2	88.0	834	10	AX090389 AX090389 Sequence
c	31	13.2	88.0	882	94	MMU276871 AJ276871 Mus muscu
c	32	13.2	88.0	909	94	MMU276516 AJ276516 Mus muscu
	33	13.2	88.0	988	7	BTBMP1 Y14605 Bos taurus
	34	13.2	88.0	1001	53	CNS06IZ1 AL400931 T7 end of
c	35	13.2	88.0	1002	45	E11419 E11419 cDNA encodi
	36	13.2	88.0	1051	53	CNS07740 AL432214 T7 end of
	37	13.2	88.0	1053	53	CNS06QTI AL411100 T7 end of
	38	13.2	88.0	1091	53	CNS06ZY7 AL422933 T3 end of
	39	13.2	88.0	1107	2	AF334165 AF334165 Mycobacte
	40	13.2	88.0	1110	88	AF073921 AF073921 Homo sapi
c	41	13.2	88.0	1114	93	HSM801875 AL136907 Homo sapi
c	42	13.2	88.0	1170	12	AB031003 AB031003 Cyanidios
	43	13.2	88.0	1171	2	AY007557 AY007557 Mycobacte
	44	13.2	88.0	1179	9	A27209 A27209 AHSV-4 S7 g
	45	13.2	88.0	1179	58	AHSVVP7 X56676 African hor

ALIGNMENTS

```
RESULT   1
AX090397
LOCUS       AX090397        26 bp    DNA             PAT       21-MAR-2001
DEFINITION  Sequence 10 from Patent WO0116169.
ACCESSION   AX090397
VERSION     AX090397.1  GI:13444254
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Worley,D.
  TITLE     Ret ligand 5 (retl5) from human and mouse
  JOURNAL   Patent: WO 0116169-A 10 08-MAR-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide"
BASE COUNT        6 a      8 c     10 g      2 t
ORIGIN


  Query Match           88.0%;  Score 13.2;  DB 10;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db      4 GCTCCAGGGGCTCCA 18
```

```
RESULT   2
AB00468S29
LOCUS       AB00468S29      84 bp    DNA             PRI       14-APR-2000
DEFINITION  Human gene for Type XIX collagen a1 chain, exon 29.
ACCESSION   AB004603
VERSION     AB004603.1  GI:2598694
KEYWORDS    Type XIX collagen a1 chain.
SEGMENT     29 of 52
SOURCE      Homo sapiens DNA, clone:MKG34.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Khaleduzzaman,M., Sumiyoshi,H., Ueki,Y., Inoguchi,K., Ninomiya,Y.
            and Yoshioka,H.
  TITLE     Structure of the human type XIX collagen (COL19A1) gene, which
            suggests it has arisen from an ancestor gene of the FACIT family
  JOURNAL   Genomics 45 (2), 304-312 (1997)
  MEDLINE   98008918
REFERENCE   2  (bases 1 to 84)
  AUTHORS   Yoshioka,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1997) to the DDBJ/EMBL/GenBank databases.
            Hidekatsu Yoshioka, Okayama University Medical School, Molecular
            Biology and Biochemistry; 2-5-1 Shikata-cho, Okayama, Okayama 700,
            Japan (E-mail:mbb@ccews.cc.okayama-u.ac.jp, Tel:086-235-7128,
            Fax:086-222-7768)
FEATURES             Location/Qualifiers
     source          1. .84
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MKG34"
     exon            16. .69
                     /gene="COL19A1"
                     /number=29
BASE COUNT       14 a     24 c     22 g     24 t
ORIGIN


  Query Match           88.0%;  Score 13.2;  DB 85;  Length 84;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db     46 ACTCCAGGGACTCCA 60
```

```
RESULT   3
G06299
LOCUS       G06299        310 bp    DNA             STS       19-OCT-1995
DEFINITION  human STS WI-6896.
ACCESSION   G06299
VERSION     G06299.1  GI:859544
KEYWORDS    STS sequence; primer; sequence tagged site.
SOURCE      human STSs derived from sequences in dbEST and the Unigene
            collection.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 310)
  AUTHORS   Hudson,T.
  TITLE     Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped ESTs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:52:00 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-9
Perfect score: 15
Sequence: 1 RCTCCANGGRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
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44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
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49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_vi:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_vi1:*
59: gb_vi2:*
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61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
69: gb_htg10:*
70: gb_htg11:*
71: gb_htg12:*
72: gb_htg13:*
73: gb_htg14:*
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81: gb_htg22:*
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90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.2	88.0	26	10	AX090397	AX090397 Sequence
	2	13.2	88.0	84	85	AB00468S29	AB004603 Human gen
	3	13.2	88.0	310	54	G06299	G06299 human STS W
c	4	13.2	88.0	324	45	E11372	E11372 cDNA encodi
	5	13.2	88.0	325	54	DM128B5S	Z71056 D. melanoga
	6	13.2	88.0	360	94	MMRARB1	X56569 Mouse RAR-b
c	7	13.2	88.0	396	9	AR064381	AR064381 Sequence
c	8	13.2	88.0	396	10	I41335	I41335 Sequence 6

```
Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    184 ACTCCAAGGACTCCA 170


RESULT  14
AAA67196
ID   AAA67196 standard; DNA; 298 BP.
XX
AC   AAA67196;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Eucalyptus grandis alpha-glucosidase DNA sequence SEQ ID NO:197.
XX
KW   Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW   plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW   transgenic plant; ds.
XX
OS   Eucalyptus grandis.
XX
PN   WO200022092-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-NZ00169.
XX
PR   13-OCT-1998;   98US-0170862.
PR   11-AUG-1999;   99US-0148426.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
PA   (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI   Bloksberg LN;
XX
DR   WPI; 2000-339328/29.
XX
PT   New genes encoding proteins involved in a plant polysaccharide
PT   biosynthetic pathway, useful for modulating or altering the
PT   polysaccharide content, composition or structure of the plant -
XX
PS   Claim 1; Page 126; 301pp; English.
XX
CC   The present invention describes isolated polynucleotides (PN) comprising
CC   a sequence selected from one of 835 nucleotide sequences given in
CC   AAA67073 to AAA67907, their (reverse) complements, sequences producing
CC   an Expectation (E) value of 0.01 or less compared to the 835 sequences,
CC   sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC   835 sequences or sequences that are degenerately equivalent or allelic
CC   to the 835 sequences. The polynucleotides are used to modify the
CC   activity of a polypeptide involved in a polysaccharide biosynthetic
CC   pathway in the plant. They are especially used to modulate or alter the
CC   polysaccharide content, composition or structure of the plant. AAB16268
CC   to AAB16340 are proteins encoded by some of the polynucleotide sequence
CC   given in the present invention.
XX
SQ   Sequence 298 BP; 77 A; 68 C; 75 G; 75 T; 3 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 298;
  Best Local Similarity   80.0%;  Pred. No. 5.2e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    101 actccaagggctcca 115


RESULT  15
AAA00475/c
ID   AAA00475 standard; cDNA; 300 BP.
XX
AC   AAA00475;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:466.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection; cancerous state; metastasis; identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675-A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US10602.
XX
PR   14-MAY-1998;   98US-0085426.
PR   15-MAY-1998;   98US-0085537.
PR   15-MAY-1998;   98US-0085696.
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-126369/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 291; 1097pp; English.
XX
CC   AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 300 BP; 108 A; 38 C; 55 G; 99 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 300;
  Best Local Similarity   80.0%;  Pred. No. 5.2e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    248 ACTCCACGGGCTCCA 234


Search completed: August 29, 2001, 20:16:43
Job time: 7424 sec
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```
CC   acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC   syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC   injury and trauma. The compounds are also useful for treating conditions
CC   such as neural degeneration where neural growth and regeneration are
CC   desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC   disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC   motor neuron disease, demyelinating disease, bacterial diseases, viral
CC   diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC   compounds are also useful for treating disorders due to damage to neural
CC   tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC   such as hemorrhage or emboli, and neural disorders such as mental
CC   retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC   palsy. The present sequence represents an atisense oligo KD2-819 used in
CC   the characterisation of genomic clones for RetL5.
XX
SQ   Sequence 26 BP; 6 A; 8 C; 10 G; 2 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 22;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db      4 gctccaggggctcca 18


RESULT  12
AAV55971/c
ID   AAV55971 standard; DNA; 204 BP.
XX
AC   AAV55971;
XX
DT   18-JAN-1999  (first entry)
XX
DE   Human cytokine receptor Zcytor4 expressed sequence tag.
XX
KW   Cytokine receptor; Zcytor4; human; cell proliferation;
KW   cell differentiation; cell adhesion; Burkitt's lymphoma;
KW   leukaemia; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9842836-A1.
XX
PD   01-OCT-1998.
XX
PF   18-MAR-1998;   98WO-US05254.
XX
PR   21-MAR-1997;   97US-0041570.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Adams RL,  Farrah TM,  Kho CJ,  Lok S,  Pownder TA;
PI   Whitmore T;
XX
DR   WPI; 1998-542279/46.
XX
PT   Human and mouse cytokine receptors, DNA and antibodies - also
PT   chimeric proteins, useful for promoting cell adhesion and diagnosing
PT   Burkitt's lymphoma and leukaemia
XX
PS   Example 1; Page 52; 66pp; English.
XX
CC   This is the nucleotide sequence of an expressed sequence tag
CC   identified during the cloning of human cytokine receptor Zcytor4
CC   cDNA (see AAV55968).  A cDNA containing 2130 bp was obtained from a
CC   human kidney cDNA library.  The DNA was transfected into
CC   Escherichia coli strain DH10b and the plasmid was designated
CC   pSL6907.  This has been used to generate probes to examine
CC   expression of Zcytor4.  The invention provides Zcytor4
CC   polynucleotides (see AAV55968) and polypepides (see AAW80754-56),
CC   expression vectors, eukaryotic host cells which express Zcytor4
CC   polypeptide, chimeric proteins comprising Zcytor4 polypeptide and
CC   an affinity tag, and antibodies that specifically bind Zcytor4.
CC   Zcytor4 may play a role in intracellular adhesion and in the
CC   regulation or development of haematopoietic cells.
XX
SQ   Sequence 204 BP; 45 A; 45 C; 55 G; 51 T; 8 other;


  Query Match             88.0%;  Score 13.2;  DB 19;  Length 204;
  Best Local Similarity   80.0%;  Pred. No. 5.2e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db     57 ACTCCAAGGACTCCA 43


RESULT  13
AAV55980/c
ID   AAV55980 standard; DNA; 211 BP.
XX
AC   AAV55980;
XX
DT   18-JAN-1999  (first entry)
XX
DE   Human cytokine receptor Zcytor4 DNA probe.
XX
KW   Cytokine receptor; Zcytor4; human; cell proliferation;
KW   cell differentiation; cell adhesion; Burkitt's lymphoma;
KW   leukaemia; diagnosis; probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9842836-A1.
XX
PD   01-OCT-1998.
XX
PF   18-MAR-1998;   98WO-US05254.
XX
PR   21-MAR-1997;   97US-0041570.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Adams RL,  Farrah TM,  Kho CJ,  Lok S,  Pownder TA;
PI   Whitmore T;
XX
DR   WPI; 1998-542279/46.
XX
PT   Human and mouse cytokine receptors, DNA and antibodies - also
PT   chimeric proteins, useful for promoting cell adhesion and diagnosing
PT   Burkitt's lymphoma and leukaemia
XX
PS   Example 1; Page 55; 66pp; English.
XX
CC   This polynucleotide was generated as a probe for the isolation of
CC   novel human cytokine receptor Zcytor4 cDNA.  It was generated by
CC   PCR amplification (see AAV55972 and AAV55972) of a human foetal kidney
CC   cDNA library.  The invention provides human and mouse cytokine
CC   receptor Zcytor4 polynucleotides (see AAV55968-69) and polypeptides
CC   (see AAW80754-57), expression vectors, eukaryotic host cells which
CC   express Zcytor4, chimeric proteins comprising a Zcytor4 polypeptide
CC   and an affinity tag, and antibodies that specifically bind Zcytor4.
CC   Zcytor4 may play a role in intracellular adhesion and in the
CC   regulation or development of haematopoietic cells.
XX
SQ   Sequence 211 BP; 57 A; 45 C; 51 G; 58 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 19;  Length 211;
  Best Local Similarity   80.0%;  Pred. No. 5.2e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      15 GCTCCAAGGGCTCCA 1


RESULT  10
AAZ90922/c
ID   AAZ90922 standard; DNA; 15 BP.
XX
AC   AAZ90922;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #150.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 45; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      15 GCTCCAGGGACTCCA 1


RESULT  11
AAF57274
ID   AAF57274 standard; DNA; 26 BP.
XX
AC   AAF57274;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Antisense oligo KD2-819 for RetL5 genomic clones characterisation.
XX
KW   Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
KW   vulnerary; nootropic; anti-HIV; neuroprotective;  antibacterial; ss;
KW   cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
XX
OS   Mus sp.
XX
PN   WO200116169-A2.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-US24111.
XX
PR   01-SEP-1999;   99US-0152024.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Worley D;
XX
DR   WPI; 2001-235091/24.
XX
PT   Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT   cell that expresses Ret and for modulating Ret signal transduction
PT   involving a cell expressing Ret polypeptide or Ret ligand polypeptide
PT   -
XX
PS   Example 5; Page 33; 76pp; English.
XX
CC   The invention relates to mouse and human Ret ligand 5 (RetL5)
CC   polypeptides. The RetL5 polypeptides can be expressed by standard
CC   recombinant methodology. The RetL5 when bound to Ret, acts as a
CC   dimerization or autophosphorylation activator. The polypeptides and their
CC   antibodies are useful for stimulating growth of or limiting damage to,
CC   Ret expressing tissue in a subject, for suppressing growth of a tumour
CC   cell that expresses Ret, for modulating Ret signal transduction involving
CC   a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion
CC   proteins containing RetL5 and antibodies are useful for stimulating renal
CC   tissue growth and/or survival, supporting renal function and minimizing
CC   damage to renal tissue after various insults, particularly for treating
```

```
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db     15 GCTCCAAGGACTCCA 1


RESULT   7
AAZ90863/c
ID   AAZ90863 standard; DNA; 15 BP.
XX
AC   AAZ90863;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #91.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 42; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db     15 ACTCCAGGGGCTCCA 1


RESULT   8
AAZ90885/c
ID   AAZ90885 standard; DNA; 15 BP.
XX
AC   AAZ90885;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #113.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db     15 GCTCCAGGGACTCCA 1


RESULT   9
AAZ90890/c
ID   AAZ90890 standard; DNA; 15 BP.
XX
AC   AAZ90890;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #118.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
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KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      15 GCTCCAGGGACTCCA 1


RESULT   5
AAZ90850/c
ID   AAZ90850 standard; DNA; 15 BP.
XX
AC   AAZ90850;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #78.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 41; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      15 GCTCCAGGGACTCCA 1


RESULT   6
AAZ90853/c
ID   AAZ90853 standard; DNA; 15 BP.
XX
AC   AAZ90853;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #81.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 41; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
```

```
PS   Claim 12; Page 52; 87pp; English.
XX
CC   5 Degenerate hybridisation probes (AAT17870-74) are based on a
CC   conserved motif (AAR92812) found in haemopoietin receptors.  The
CC   probes are used in the identification and/or cloning of genes
CC   coding for novel haemopoietin receptors, e.g. the murine
CC   interleukin-11 (IL-11) receptor alpha chain gene (AAT17868).  Such
CC   receptors are defined by their ability to hybridise to the
CC   probes under medium stringency conditions.
XX
SQ   Sequence 15 BP; 2 A; 6 C; 2 G; 2 T; 3 other;


  Query Match             88.0%;  Score 13.2;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          |||||||||||||||
Db      1 rctccanggrctcca 15


RESULT   2
AAZ59273/c
ID   AAZ59273 standard; DNA; 15 BP.
XX
AC   AAZ59273;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #16.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 38; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 3 A; 2 C; 6 G; 4 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db     15 ACTCCATGGACTCCA 1


RESULT   3
AAZ90833/c
ID   AAZ90833 standard; DNA; 15 BP.
XX
AC   AAZ90833;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #61.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;


  Query Match             88.0%;  Score 13.2;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :|||||  ||:|||||
Db     15 ACTCCAGGGGCTCCA 1


RESULT   4
AAZ90834/c
ID   AAZ90834 standard; DNA; 15 BP.
XX
AC   AAZ90834;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #62.
XX
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:43 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-9
Perfect score: 15
Sequence: 1 RCTCCANGGRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.2	88.0	15	17	AAT17873	Haemopoietin recep
c	2	13.2	88.0	15	21	AAZ59273	Human NR8 gene pro
c	3	13.2	88.0	15	21	AAZ90833	Human NR8 gene pro
c	4	13.2	88.0	15	21	AAZ90834	Human NR8 gene pro
c	5	13.2	88.0	15	21	AAZ90850	Human NR8 gene pro
c	6	13.2	88.0	15	21	AAZ90853	Human NR8 gene pro
c	7	13.2	88.0	15	21	AAZ90863	Human NR8 gene pro
c	8	13.2	88.0	15	21	AAZ90885	Human NR8 gene pro
c	9	13.2	88.0	15	21	AAZ90890	Human NR8 gene pro
c	10	13.2	88.0	15	21	AAZ90922	Human NR8 gene pro
	11	13.2	88.0	26	22	AAF57274	Antisense oligo KD
c	12	13.2	88.0	204	19	AAV55971	Human cytokine rec
c	13	13.2	88.0	211	19	AAV55980	Human cytokine rec
	14	13.2	88.0	298	21	AAA67196	Eucalyptus grandis
c	15	13.2	88.0	300	21	AAA00475	Human colon cancer
c	16	13.2	88.0	324	17	AAT33517	G-CSF receptor lig
c	17	13.2	88.0	349	21	AAZ42586	Human 5' EST isola
c	18	13.2	88.0	396	16	AAQ84638	Squirrel Monkey co
c	19	13.2	88.0	396	16	AAQ99109	SQMCIP full-length
c	20	13.2	88.0	396	16	AAT03334	Ly-6 terminal CIP
c	21	13.2	88.0	639	17	AAT33515	Mouse G-CSF recept
c	22	13.2	88.0	725	21	AAA02109	Human colon cancer
c	23	13.2	88.0	765	17	AAT35141	DNA encoding cytok
c	24	13.2	88.0	783	22	AAF57273	Mouse RetL5 altern
c	25	13.2	88.0	792	22	AAF31057	Murine EST AU03593
c	26	13.2	88.0	795	22	AAF57271	Mouse RetL5 polype
c	27	13.2	88.0	795	22	AAC84378	Human TANGO 204 po
c	28	13.2	88.0	795	22	AAC84386	Mouse TANGO 204 po
c	29	13.2	88.0	834	22	AAF57270	Mouse RetL5 polype
c	30	13.2	88.0	1002	17	AAT35137	DNA encoding cytok
c	31	13.2	88.0	1019	20	AAZ28259	Murine glial deriv
	32	13.2	88.0	1178	13	AAQ30130	Gene for AHSV. Af
c	33	13.2	88.0	1293	22	AAC84385	Mouse TANGO 204 po
c	34	13.2	88.0	1293	22	AAC84396	Mouse TANGO 204 va
c	35	13.2	88.0	1293	22	AAC84397	Mouse TANGO 204 va
c	36	13.2	88.0	1293	22	AAC84398	Mouse TANGO 204 va
	37	13.2	88.0	1590	19	AAV63614	DNA sequence encod
	38	13.2	88.0	1590	19	AAV63541	DNA sequence encod
	39	13.2	88.0	1607	21	AAF15587	Human prostate can
c	40	13.2	88.0	1656	19	AAV02978	Human interleukin-
c	41	13.2	88.0	1874	21	AAF21936	Human breast and o
	42	13.2	88.0	1974	21	AAC77172	Human ORFX ORF2727
c	43	13.2	88.0	1998	20	AAZ00367	Nucleotide sequenc
c	44	13.2	88.0	2087	20	AAZ00343	Nucleotide sequenc
c	45	13.2	88.0	2166	20	AAZ00379	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAT17873
ID AAT17873 standard; DNA; 15 BP.
XX
AC AAT17873;
XX
DT 21-MAY-1996 (first entry)
XX
DE Haemopoietin receptor probe HYB4.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN WO9607737-A1.
XX
PD 14-MAR-1996.
XX
PF 05-SEP-1995; 95WO-AU00578.
XX
PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ;
XX
DR WPI; 1996-171612/17.
XX
PT Nucleic acid encoding haemopoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists
XX

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db     66 GCTCCAGGGACTCCA 52
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RESULT 15
D45552
LOCUS D45552 235 bp mRNA EST 20-FEB-1995
DEFINITION HUMGS02739 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA 3', mRNA sequence.
ACCESSION D45552
VERSION D45552.1 GI:662506
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 235)
AUTHORS Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.
TITLE An expression profile of active genes in human lung
JOURNAL DNA Research 1, 279-287 (1994)
MEDLINE 95236275
COMMENT Contact: Kohichi Itoh
Institute for Molecular and Cellular Biology
Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
FEATURES Location/Qualifiers
source 1. .235
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Adult human lung, 3' directed MboI"
BASE COUNT 41 a 85 c 55 g 48 t 6 others
ORIGIN

Query Match 88.0%; Score 13.2; DB 156; Length 235;
Best Local Similarity 80.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    197 GCTCCAGGGACTCCA 211
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Search completed: August 29, 2001, 19:22:17
Job time: 24140 sec

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            Please visit our web site (http://genome.rtc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5033406C17"
                     /clone_lib="RIKEN full-length enriched, 11 days pregnant
                     adult female ovary and uterus"
                     /sex="female"
                     /tissue_type="ovary and uterus"
                     /dev_stage="11 days pregnant, adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI."
BASE COUNT       74 a     51 c     44 g     61 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 28;  Length 230;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db     92 ACTCCATGGACTCCA 106


RESULT  13
AI234857/c
LOCUS       AI234857      232 bp    mRNA            EST       31-JAN-1999
DEFINITION  EST231419 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
            ROVCI69 3' end, mRNA sequence.
ACCESSION   AI234857
VERSION     AI234857.1  GI:3828363
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 232)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .232
                     /organism="Rattus sp."
                     /db_xref="ATCC (inhost):2040521"
                     /db_xref="taxon:10118"
                     /clone="ROVCI69"
                     /clone_lib="Normalized rat ovary, Bento Soares"
                     /note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT       61 a     45 c     66 g     60 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 17;  Length 232;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RCTCCANGGRCTCCA 15
          :||||| ||:|||||
Db    216 GCTCCAGGGACTCCA 202


RESULT  14
AA587324/c
LOCUS       AA587324      233 bp    mRNA            EST       26-SEP-1997
DEFINITION  nn78e01.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090008 3',
            mRNA sequence.
ACCESSION   AA587324
VERSION     AA587324.1  GI:2398138
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 233)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 545   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 153.
FEATURES             Location/Qualifiers
     source          1. .233
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1090008"
                     /clone_lib="NCI_CGAP_Co9"
                     /tissue_type="colon tumor RER+"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     RER+ colon tumor, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is not normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                     ). "
BASE COUNT       45 a     51 c     79 g     58 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 9;  Length 233;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+03;
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```
Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db     205 ACTCCATGGGCTCCA 191


RESULT  11
AV282369/c
LOCUS       AV282369      227 bp    mRNA            EST       08-NOV-1999
DEFINITION  AV282369 RIKEN full-length enriched, adult male testis (DH10B) Mus
            musculus cDNA clone 4933429K08 3' similar to AB029026 Homo sapiens
            mRNA for KIAA1103 protein, mRNA sequence.
ACCESSION   AV282369
VERSION     AV282369.1  GI:6275118
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 227)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
            ,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
            Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,
            Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
            Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
            ,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .227
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="4933429K08"
                     /clone_lib="RIKEN full-length enriched, adult male testis
                     (DH10B)"
                     /sex="male"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT       71 a     46 c     52 g     58 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 28;  Length 227;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      29 ACTCCAAGGACTCCA 15


RESULT  12
AV288298
LOCUS       AV288298      230 bp    mRNA            EST       09-NOV-1999
DEFINITION  AV288298 RIKEN full-length enriched, 11 days pregnant adult female
            ovary and uterus Mus musculus cDNA clone 5033406C17, mRNA sequence.
ACCESSION   AV288298
VERSION     AV288298.1  GI:6298802
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
            ,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
            Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,
            Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
            Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome-res@rtc.riken.go.jp,
            URL:http://genome.rtc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
            ,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
```

GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
BASE COUNT 47 a 49 c 53 g 53 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 29; Length 202;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 60 GCTCCAGGGGCTCCA 46

RESULT 9
BF380015
LOCUS BF380015 221 bp mRNA EST 27-NOV-2000
DEFINITION MR0-UT0047-080900-201-d07 UT0047 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF380015
VERSION BF380015.1 GI:11369140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 221)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-UT0047-080900-201-d07&t3=2000-09-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 56
High quality sequence stop: 219.
FEATURES Location/Qualifiers
source 1. .221
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0047"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 69 a 45 c 57 g 50 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 148; Length 221;
Best Local Similarity 80.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 200 GCTCCATGGACTCCA 214

RESULT 10
AW462741/c
LOCUS AW462741 226 bp mRNA EST 24-FEB-2000
DEFINITION BP230010A20B6 Soares normalized bovine placenta Bos taurus cDNA clone BP230010A20B6 5', mRNA sequence.
ACCESSION AW462741
VERSION AW462741.1 GI:7032909
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 226)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 226 Std Error: 0.00
Plate: BP230010A20 row: B column: 6
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 226.
FEATURES Location/Qualifiers
source 1. .226
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP230010A20B6"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
BASE COUNT 52 a 49 c 60 g 65 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 116; Length 226;
Best Local Similarity 80.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 55 a 46 c 49 g 48 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 120; Length 198;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 67 ACTCCAAGGACTCCA 81

RESULT 7
AA163051
LOCUS AA163051 199 bp mRNA EST 12-FEB-1997
DEFINITION ms24a10.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:607866 5', mRNA sequence.
ACCESSION AA163051
VERSION AA163051.1 GI:1739014
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 199)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:373298
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 183.
FEATURES Location/Qualifiers
source 1. .199
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:607866"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT 47 a 39 c 49 g 64 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 3; Length 199;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 153 GCTCCATGGGCTCCA 167

RESULT 8
AV340647/c
LOCUS AV340647 202 bp mRNA EST 11-NOV-1999
DEFINITION AV340647 RIKEN full-length enriched, adult male olfactory bulb Mus musculus cDNA clone 6430516D09 3', mRNA sequence.
ACCESSION AV340647
VERSION AV340647.1 GI:6380699
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 202)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .202
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6430516D09"
/clone_lib="RIKEN full-length enriched, adult male olfactory bulb"
/sex="male"
/tissue_type="olfactory brain"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

```
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .182
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2610207N04"
                     /clone_lib="Mus musculus C57BL/6J 10-day embryo"
                     /sex="mixed"
                     /dev_stage="10-day embryo"
BASE COUNT       58 a     40 c     37 g     47 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 25;  Length 182;
  Best Local Similarity   80.0%;  Pred. No. 5.4e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      42 ACTCCATGGACTCCA 56


RESULT   5
AI933508/c
LOCUS       AI933508      187 bp    mRNA            EST       07-MAR-2000
DEFINITION  wm74e06.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2441698 3',
            mRNA sequence.
ACCESSION   AI933508
VERSION     AI933508.1  GI:5672245
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 187)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1894    Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 133.
FEATURES             Location/Qualifiers
     source          1. .187
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2441698"
                     /clone_lib="NCI_CGAP_Ut2"
                     /tissue_type="moderately-differentiated endometrial
                     adenocarcinoma, 3 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.85 kb. Life Technologies catalog #:
                     11539-012"
BASE COUNT       36 a     42 c     62 g     47 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 103;  Length 187;
  Best Local Similarity   80.0%;  Pred. No. 5.4e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
           :||||| ||:|||||
Db      55 GCTCCAGGGACTCCA 41


RESULT   6
AW804893
LOCUS       AW804893 -     198 bp    mRNA            EST       16-MAY-2000
DEFINITION  QV4-UM0094-280300-152-a01 UM0094 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW804893
VERSION     AW804893.1  GI:7856672
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 198)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV4-UM0094-280
            300-152-a01&t3=2000-03-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 198.
FEATURES             Location/Qualifiers
     source          1. .198
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="UM0094"
                     /dev_stage="Adult"
                     /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
```

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 632 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 107.

FEATURES Location/Qualifiers
source 1. .151
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2011202"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 33 a 37 c 50 g 31 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 19; Length 151;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 42 GCTCCAGGGACTCCA 28

RESULT 3
BB593914/c
LOCUS BB593914 170 bp mRNA EST 30-NOV-2000
DEFINITION BB593914 RIKEN full-length enriched, 4 days neonate male adipose Mus musculus cDNA clone B430304H06 5', mRNA sequence.
ACCESSION BB593914
VERSION BB593914.1 GI:11490516
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 170)
AUTHORS Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .170
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B430304H06"
/clone_lib="RIKEN full-length enriched, 4 days neonate male adipose"
/sex="male"
/tissue_type="adipose"
/dev_stage="4 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 229.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 34 a 54 c 50 g 32 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 161; Length 170;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 58 GCTCCAGGGGCTCCA 44

RESULT 4
AV118281
LOCUS AV118281 182 bp mRNA EST 30-JUN-1999
DEFINITION AV118281 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610207N04, mRNA sequence.
ACCESSION AV118281
VERSION AV118281.1 GI:5300432
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 182)
AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13.2	88.0	100	10	AA644792	AA644792 vs82d07.r
c 2	13.2	88.0	151	19	AI371456	AI371456 qy06c02.x
c 3	13.2	88.0	170	161	BB593914	BB593914 BB593914
4	13.2	88.0	182	25	AV118281	AV118281 AV118281
c 5	13.2	88.0	187	103	AI933508	AI933508 wm74e06.x
6	13.2	88.0	198	120	AW804893	AW804893 QV4-UM009
7	13.2	88.0	199	3	AA163051	AA163051 ms24a10.r
c 8	13.2	88.0	202	29	AV340647	AV340647 AV340647
9	13.2	88.0	221	148	BF380015	BF380015 MR0-UT004
c 10	13.2	88.0	226	116	AW462741	AW462741 BP230010A
c 11	13.2	88.0	227	28	AV282369	AV282369 AV282369
12	13.2	88.0	230	28	AV288298	AV288298 AV288298
c 13	13.2	88.0	232	17	AI234857	AI234857 EST231419
c 14	13.2	88.0	233	9	AA587324	AA587324 nn78e01.s
15	13.2	88.0	235	156	D45552	D45552 HUMGS02739
16	13.2	88.0	236	2	AA089075	AA089075 mo63a01.r
17	13.2	88.0	237	188	T03328	T03328 IB1253 Infa
c 18	13.2	88.0	240	156	C12571	C12571 C12571 Yuji
c 19	13.2	88.0	246	158	H32365	H32365 EST107377 R
20	13.2	88.0	250	17	AI185438	AI185438 qe53d09.x
21	13.2	88.0	250	127	BB180104	BB180104 BB180104
22	13.2	88.0	251	157	F37625	F37625 HSPD05393 H
23	13.2	88.0	253	10	AA653297	AA653297 ag65c06.s
c 24	13.2	88.0	255	157	F01487	F01487 HSC04D122 n
c 25	13.2	88.0	256	5	AA340930	AA340930 EST46241
c 26	13.2	88.0	260	168	BF714533	BF714533 mab01e01.
c 27	13.2	88.0	262	131	BB313512	BB313512 BB313512
c 28	13.2	88.0	264	21	AI547450	AI547450 UI-R-C3-s
c 29	13.2	88.0	268	8	AA494436	AA494436 ne28d04.s
c 30	13.2	88.0	271	22	AI606963	AI606963 vw36f02.x
c 31	13.2	88.0	271	146	BF228467	BF228467 BP250008B
32	13.2	88.0	275	134	BB461437	BB461437 BB461437
33	13.2	88.0	275	138	BE631643	BE631643 uu63a05.y
c 34	13.2	88.0	276	4	AA288582	AA288582 mp15g05.r
35	13.2	88.0	276	168	BF714534	BF714534 mab01e01.
36	13.2	88.0	280	146	BF290833	BF290833 EST455424
c 37	13.2	88.0	283	240	AZ227737	AZ227737 RPCI-23-8
c 38	13.2	88.0	285	158	H34301	H34301 EST111113 R
39	13.2	88.0	286	157	F21363	F21363 HSPD05876 H
c 40	13.2	88.0	287	147	BF363285	BF363285 CM2-NN011
c 41	13.2	88.0	288	143	BF010839	BF010839 NXCI_095_
c 42	13.2	88.0	289	14	AA963063	AA963063 UI-R-E1-f
43	13.2	88.0	295	171	BF931642	BF931642 IL2-NT020
44	13.2	88.0	296	12	AA822320	AA822320 vw36f02.r
45	13.2	88.0	296	20	AI465630	AI465630 vw36f02.y

ALIGNMENTS

```
RESULT   1
AA644792
LOCUS       AA644792      100 bp    mRNA            EST       28-OCT-1997
DEFINITION  vs82d07.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
            IMAGE:1152781 5' similar to gb:M80359 PUTATIVE
            SERINE/THREONINE-PROTEIN KINASE P78 (HUMAN); gb:X70764 M.musculus
            mRNA for serine/threonine protein kinase (MOUSE);, mRNA sequence.
ACCESSION   AA644792
VERSION     AA644792.1  GI:2571221
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:625989
            Trace considered overall poor quality
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Mus musculus"
                     /strain="C3H"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1152781"
                     /clone_lib="Barstead mouse myotubes MPLRB5"
                     /cell_line="C2C12"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [AATTCGGATCCTTG], digested with Not I and cloned into the
                     Not I and Eco RI sites of the modified pT7T3 vector.
                     Library constructed by Bob Barstead. The C2C12 cell line
                     (available from ATCC, catalog # CRL-1772) differentiates
                     rapidly, forming contractile myotubes and producing
                     characteristic muscle proteins. "
BASE COUNT       24 a     27 c     29 g     20 t
ORIGIN


  Query Match             88.0%;  Score 13.2;  DB 10;  Length 100;
  Best Local Similarity   80.0%;  Pred. No. 5.1e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RCTCCANGGRCTCCA 15
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Db      48 GCTCCATGGACTCCA 62


RESULT   2
AI371456/c
LOCUS       AI371456      151 bp    mRNA            EST       15-FEB-1999
DEFINITION  qy06c02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2011202 3',
            mRNA sequence.
ACCESSION   AI371456
VERSION     AI371456.1  GI:4150209
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 151)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
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258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:14 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-9
Perfect score: 15
Sequence: 1 RCTCCANGGRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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     exon            293. .323
                     /gene="IL-12RB1"
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                     /number=7
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     intron          872. .1187
                     /gene="IL-12RB1"
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ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    849 GCTCCACTTGCTCCA 835


RESULT  15
AF072549
LOCUS       AF072549     1290 bp    mRNA            VRT       15-AUG-1998
DEFINITION  Danio rerio transcription factor (Pax8) mRNA, partial cds.
ACCESSION   AF072549
VERSION     AF072549.1  GI:3420034
KEYWORDS    .
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 1290)
  AUTHORS   Pfeffer,P.L., Gerster,T., Lun,K., Brand,M. and Busslinger,M.
  TITLE     Characterization of three novel members of the zebrafish Pax2/5/8
            family: dependency of Pax5 and Pax8 expression on the Pax2.1 (noi)
            function
  JOURNAL   Development 125 (16), 3063-3074 (1998)
  MEDLINE   98337826
REFERENCE   2  (bases 1 to 1290)
  AUTHORS   Pfeffer,P.L. and Busslinger,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUN-1998) Institute of Molecular Pathology, Dr.
            Bohr-Gasse 7, Vienna A-1030, Austria
FEATURES             Location/Qualifiers
     source          1. .1290
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
     gene            <1. .1290
                     /gene="Pax8"
     CDS             <1. .1290
                     /gene="Pax8"
                     /codon_start=1
                     /product="transcription factor"
                     /protein_id="AAC31813.1"
                     /db_xref="GI:3420035"
                     /translation="VNGRPLPEVIRQRIVDMAHQGVRPCDISRQLRVSHGCVSKILGR
                     YYETGSIKPGVIGGSKPKVATPKVVEKIAEYKRQNPTMFAWEIRDRLLAEGVCDGDTV
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                     LLGITQTTADGKRGHDDSDQESCRHSVDSQGSGGGARKQLRTEHFPSAALDCGFERHY
                     SSDSFSQSKAEQQLYPLALMNPGLDEGKGASSISRNLAAHQGYAVVTEALQPLPLCLK
                     QEVSPEVNSLSPSPHIISGSAFLDLSAISSPSSAPVASSCGSAHLSHGFSSFSHHAPV
                     HGQFSSPSLMAGREVASSMLPGYPPHIPTAQTGFSSSTIAGMVSAPEYTGQSYSHPAY
                     SSYSEAWRFTNSSILGSPYYYSFANRPPPPAGAFDHL"
BASE COUNT      282 a    427 c    353 g    228 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 8;  Length 1290;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    458 GCTCCACTTACTCCA 472


Search completed: August 29, 2001, 19:52:03
Job time: 17241 sec
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1063)
  AUTHORS   Hardies,S.C.
  TITLE     Members of the Mouse retrovirus-related repetitive sequence MuERVC
            recovered from C57BL/6J and SPRET/Ei
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1063)
  AUTHORS   Hardies,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-1998) Biochemistry, Univ. of Texas Health Science
            Center at San Antonio, 7703 Floyd Curl Dr., San Antonio, TX 78284,
            USA
FEATURES             Location/Qualifiers
     source          1. .1063
                     /organism="Mus musculus domesticus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10092"
                     /clone="M8"
     repeat_region   <1. .>1063
                     /note="similar to the gag-pol of Moloney Murine Leukemia
                     virus"
                     /rpt_type=dispersed
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BASE COUNT      347 a    196 c    297 g    223 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 94;  Length 1063;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     79 ACTCCATTTGCTCCA 65


RESULT  13
MUSIL2RGAM/c
LOCUS       MUSIL2RGAM   1165 bp    mRNA            ROD       01-FEB-2000
DEFINITION  Mouse mRNA for mouse IL-2R gamma, complete cds.
ACCESSION   D13821
VERSION     D13821.1  GI:436045
KEYWORDS    IL-2 receptor; cytokine receptor family; gammachain; mouse IL-2R
            gamma.
SOURCE      Mus musculus (strain:C57BL16) spleen cDNA to mRNA, clone_lib:mouse
            spleen cell cDNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1165)
  AUTHORS   Kobayashi,N., Nakagawa,S., Minami,Y., Taniguchi,T. and Kono,T.
  TITLE     Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
            gamma
  JOURNAL   Gene 130 (2), 303-304 (1993)
  MEDLINE   93366191
REFERENCE   2  (bases 1 to 1165)
  AUTHORS   Taniguchi,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1992) to the DDBJ/EMBL/GenBank databases.
            Tadatsugu Taniguchi, Osaka University, Institute for Mol. and Cell.
            Biology; Suita-shi, Osaka 565, Japan (Tel:06-877-5289,
            Fax:06-878-9846)
COMMENT     Submitted (04-DEC-1992) to DDBJ by:
            Tadatsugu Taniguchi
            Institute for Molecular and
            Cellular Biology, Osaka University
            1-3 Yamadaoka
            Suita-shi, Osaka 565
            Japan
            Phone:  06-877-5289
            Fax:    06-878-9846.
FEATURES             Location/Qualifiers
     source          1. .1165
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                     /strain="C57BL16"
                     /db_xref="taxon:10090"
                     /clone_lib="mouse spleen cell cDNA"
                     /tissue_type="spleen"
     sig_peptide     8. .73
                     /gene="mouse IL-2R gamma"
     CDS             8. .1117
                     /gene="mouse IL-2R gamma"
                     /codon_start=1
                     /product="mouse IL-2R gamma precursor"
                     /protein_id="BAA02974.1"
                     /db_xref="GI:436046"
                     /translation="MLKLLLSPRSFLVLQLLLLRAGWSSKVLMSSANEDIKADLILTS
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                     IPPKGGALGEGPGGSPCSLHSPYWPPPCYSLKPEA"
     gene            8. .1117
                     /gene="mouse IL-2R gamma"
     mat_peptide     74. .1114
                     /gene="mouse IL-2R gamma"
                     /product="mouse IL-2R gamma"
BASE COUNT      308 a    292 c    276 g    289 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 94;  Length 1165;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|.||||
Db    733 GCTCCATTTACTCCA 719


RESULT  14
HSA297692/c
LOCUS       HSA297692    1187 bp    DNA             PRI       30-SEP-2000
DEFINITION  Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain,
            exons 6-7.
ACCESSION   AJ297692
VERSION     AJ297692.1  GI:10443211
KEYWORDS    IL-12 receptor beta1 chain; IL-12RB1 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1187)
  AUTHORS   Elloumi-Zghal,H., Abdelhak,S. and Dellagi,K.
  TITLE     Genomic structure of IL12RB1 gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1187)
  AUTHORS   Abdelhak,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2000) Abdelhak S., Immunology, Institut Pasteur
            de Tunis, BP74 13, Place Pasteur, Tunis, 1002, TUNISIA
FEATURES             Location/Qualifiers
     source          1. .1187
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                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.1"
     intron          1. .292
                     /gene="IL-12RB1"
                     /number=5
     repeat_region   1. .206
                     /rpt_family="Alu-Jb"
                     /rpt_type=DISPERSED
     gene            1. .1187
                     /gene="IL-12RB1"
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ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 14;  Length 979;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    425 ACTCCATTTACTCCA 439


RESULT 10
CEU21854/c
LOCUS       CEU21854     1025 bp    DNA             INV       14-FEB-1996
DEFINITION  Caenorhabditis elegans cCAF1 protein gene, complete cds.
ACCESSION   U21854
VERSION     U21854.1  GI:726133
KEYWORDS    .
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 1025)
  AUTHORS   Draper,M.P., Salvadore,C. and Denis,C.L.
  TITLE     Identification of a mouse protein whose homolog in Saccharomyces
            cerevisiae is a component of the CCR4 transcriptional regulatory
            complex
  JOURNAL   Mol. Cell. Biol. 15 (7), 3487-3495 (1995)
  MEDLINE   95311945
REFERENCE   2  (bases 1 to 1025)
  AUTHORS   Salvadore,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-1995) Christopher Salvadore, Biochemistry
            Department, University of New Hampshire, Main Syreet, Durham, NH
            03824, USA
FEATURES             Location/Qualifiers
     source          1. .1025
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                     /db_xref="taxon:6239"
     CDS             28. .960
                     /note="C.elegans CCR4 associated factor 1"
                     /codon_start=1
                     /product="cCAF1 protein"
                     /protein_id="AAA87454.1"
                     /db_xref="GI:726134"
                     /translation="MASSSSGGAGGAGGASGAPEVKIHNVYMSNVEEEFARIRGFVED
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                     GDVWQFNFNFSFAEDMFSHESVEMLRQAGIDFTLLQNNGIPTAVFGELLTTSGLITDP
                     RITWLTFSSGYDFGYLLKSITLGDLPKEESTFFMCHKTLFPTSFDIKILLRTPNCASA
                     KLKGGLQEVADQLDVKRQGVRHQAGSDALLTAATFFKIKKQFFGDNWNQIAPLICGHM
                     FGLGSSLSLFHSSGSTSRLGDETPQGLIGVPQQA"
BASE COUNT      276 a    240 c    240 g    269 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 6;  Length 1025;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     80 GCTCCACTTGCTCCA 66


RESULT 11
PT4G11A/c
LOCUS       PT4G11A      1034 bp    DNA             PHG       28-APR-1993
DEFINITION  Bacteriophage T4D gene 11 encoding baseplate structural protein
            (gp11) complete cds, gene 10, 3' end, and gene 12, 5' end.
ACCESSION   M26253
VERSION     M26253.1  GI:215856
KEYWORDS    baseplate structural protein; gp10 gene; gp11 gene; gp12 gene.
SOURCE      Bacteriophage T4 DNA, clone pJZ1 and pBB1.
  ORGANISM  Bacteriophage T4
            Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
            T4-like phages.
REFERENCE   1  (bases 1 to 1034)
  AUTHORS   Barrett,B.K. and Berget,P.B.
  TITLE     Laboratory methods using transposon Tn5 insertions to sequence
            bacteriophage T4 gene 11
  JOURNAL   DNA 8, 287-295 (1989)
  MEDLINE   89356257
COMMENT     Draft entry and computer readable copy of sequence [1] kindly
            provided by P.B.Berget, 20-JUL-1989.
            The reading frame for gp12 is in disagreement with Selivanov et
            al., (Accession #X06792).
FEATURES             Location/Qualifiers
     source          1. .1034
                     /organism="Bacteriophage T4"
                     /db_xref="taxon:10665"
     CDS             <1. .207
                     /note="gp10 protein"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA32493.1"
                     /db_xref="GI:215857"
                     /translation="TETDEEVLIVDENGSVIVGGCQYDPDESGPIYTKYREAKASTNS
                     THTPPTSITNIQPYITVYRWIRIA"
     CDS             207. .866
                     /note="baseplate structural protein (gp11)"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA32494.1"
                     /db_xref="GI:215858"
                     /translation="MSLLNNKAGVISRLADFLGFRPKTGDIDVMNRQSVGSVTISQLA
                     KGFYEPNIESAINDVHNFSIKDVGTIITNKTGVSPEGVSQTDYWAFSGTVTDDSLPPG
                     SPITVLVFGLPVSATTGMTAIEFVAKVRVALQEAIASFTAINSYKDHPTDGSKLEVTY
                     LDNQKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQQTPTVFYHFERT
                     A"
     variation       822
                     /note="c in wild type; t in amber mutants N108 and N93"
     variation       825
                     /note="c in wild type; t in amber mutants N128, NG115 and
                     NG369"
     CDS             863. .>1034
                     /note="gp12 protein"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA32495.1"
                     /db_xref="GI:553024"
                     /translation="MSNNTYQHVSNESRYVKFDPTDTNFPPEITDVQAAIAAISPAGV
                     NGVPDASSTTKGI"
BASE COUNT      332 a    191 c    186 g    325 t
ORIGIN      90 kb on genomic map.


  Query Match             92.0%;  Score 13.8;  DB 11;  Length 1034;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db   1002 ACTCCATTTACTCCA 988


RESULT 12
AF064721/c
LOCUS       AF064721     1063 bp    DNA             ROD       21-MAY-1998
DEFINITION  Mus musculus domesticus clone M8 repetitive sequence MuERVC.
ACCESSION   AF064721
VERSION     AF064721.1  GI:3142724
KEYWORDS    .
SOURCE      western European house mouse.
  ORGANISM  Mus musculus domesticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
BASE COUNT      203 a    181 c    168 g    193 t      3 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 53;  Length 748;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     46 GCTCCACTTACTCCA 32


RESULT   7
AX053546/c
LOCUS       AX053546      783 bp    DNA             PAT       13-JAN-2001
DEFINITION  Sequence 312 from Patent WO0073801.
ACCESSION   AX053546
VERSION     AX053546.1  GI:12227865
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   Obata,Y.
  TITLE     Breast, gastric and prostate cancer associated antigens and uses
            therefor
  JOURNAL   Patent: WO 0073801-A 312 07-DEC-2000;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      255 a    147 c    160 g    216 t      5 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 9;  Length 783;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     98 GCTCCATTTGCTCCA 84


RESULT   8
CNS01EI0
LOCUS       CNS01EI0      900 bp    DNA             STS       17-FEB-2000
DEFINITION  Anopheles gambiae STS SP6 end of clone 02F01 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            sequence tagged site.
ACCESSION   AL140569
VERSION     AL140569.1  GI:6998687
KEYWORDS    STS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 900)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="02F01"
                     /clone_lib="NotreDame1"
                     /note="end : SP6"
BASE COUNT      263 a    169 c    159 g    307 t      2 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 53;  Length 900;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    251 GCTCCATTTACTCCA 265


RESULT   9
RSM390345
LOCUS       RSM390345     979 bp    DNA             PLN       09-NOV-2000
DEFINITION  Reissekia smilacina chloroplast partial tRNA-Leu(UAA) and tRNA-Phe
            genes and intergenic spacer, IGS.
ACCESSION   AJ390345
VERSION     AJ390345.1  GI:9968789
KEYWORDS    IGS; intergenic spacer; transfer RNA-Leu (UAA); transfer RNA-Phe;
            tRNA-Leu (UAA) gene; tRNA-Phe gene.
SOURCE      Reissekia smilacina.
  ORGANISM  Chloroplast Reissekia smilacina
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
            Rosales; Rhamnaceae; Reissekia.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   Richardson,J.E., Fay,M.F., Cronk,Q.C., Bowman,D. and Chase,M.W.
  TITLE     A phylogenetic analysis of Rhamnaceae using rbcL and trnL-F plastid
            DNA sequences
  JOURNAL   Am. J. Bot. 87 (9), 1309-1324 (2000)
  PUBMED    10991902
REFERENCE   2  (bases 1 to 979)
  AUTHORS   Richardson,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-OCT-1999) Richardson J.E., Herbarium, Royal Botanic
            Garden, Edinburgh, 20A Inverleith Row, Edinburgh, EH3 5LR, UNITED
            KINGDOM
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="Reissekia smilacina"
                     /organelle="plastid:chloroplast"
                     /db_xref="taxon:106700"
                     /country="Brazil"
     tRNA            <1. .596
                     /gene="tRNA-Leu(UAA)"
                     /product="transfer RNA-Leu(UAA)"
     intron          1. .546
                     /gene="tRNA-Leu(UAA)"
     gene            1. .596
                     /gene="tRNA-Leu(UAA)"
     exon            547. .596
                     /gene="tRNA-Leu(UAA)"
     misc_feature    597. .945
                     /note="intergenic spacer, IGS"
     tRNA            946. .979
                     /gene="tRNA-Phe"
                     /product="transfer RNA-Phe"
     gene            946. .979
                     /gene="tRNA-Phe"
BASE COUNT      339 a    184 c    169 g    287 t
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ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 95;  Length 179;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    137 GCTCCATTTACTCCA 123


RESULT   4
LAU72036/c
LOCUS       LAU72036      271 bp    DNA             INV       30-NOV-1996
DEFINITION  Leptothorax acervorum microsatellite LXA GA 1, complete sequence.
ACCESSION   U72036
VERSION     U72036.1  GI:1695895
KEYWORDS    .
SOURCE      Leptothorax acervorum.
  ORGANISM  Leptothorax acervorum
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
            Aculeata; Formicidae; Myrmicinae; Leptothorax.
REFERENCE   1  (bases 1 to 271)
  AUTHORS   Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
  TITLE     Parentage, reproductive skew and queen turnover in a multiple-queen
            ant analysed with microsatellites
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 271)
  AUTHORS   Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-1996) Conservation Genetics Group, Institute of
            Zoology, Regent's Park, London NW1 4RY, UK
FEATURES             Location/Qualifiers
     source          1. .271
                     /organism="Leptothorax acervorum"
                     /db_xref="taxon:33409"
     repeat_region   98. .172
                     /note="LXA GA 1"
                     /rpt_family="microsatellite"
                     /rpt_type=tandem
                     /rpt_unit=ag
BASE COUNT       79 a     50 c    101 g     41 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 6;  Length 271;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    211 GCTCCACTTGCTCCA 197


RESULT   5
AF227552/c
LOCUS       AF227552      487 bp    mRNA            PRI       01-JUN-2000
DEFINITION  Macaca mulatta interleukin-12 receptor (IL-12R) mRNA, partial cds.
ACCESSION   AF227552
VERSION     AF227552.1  GI:8132798
KEYWORDS    .
SOURCE      rhesus monkey.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 487)
  AUTHORS   Arredondo,J.
  TITLE     Cytokine Signal Transduction Genes from Rhesus Macaques
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 487)
  AUTHORS   Arredondo,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) California Regional Primate Research
            Center, University of California-Davis, One Shields Avenue, Davis,
            CA 95616, USA
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Macaca mulatta"
                     /db_xref="taxon:9544"
                     /cell_type="peripheral blood mononuclear cells"
     gene            <1. .>487
                     /gene="IL-12R"
     CDS             <1. .>487
                     /gene="IL-12R"
                     /note="membrane receptor"
                     /codon_start=3
                     /product="interleukin-12 receptor"
                     /protein_id="AAF73397.1"
                     /db_xref="GI:8132799"
                     /translation="GPQDDDTESCLCPLEMNVAQEFQLRRRRLGSQGSSWSKWSSPVC
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                     LSCPCKAKATRTLPLEKMPYLSGAATMWLVISSNRFGLAQTRRGTFLLTPTQKPGVLN
                     IT"
BASE COUNT      106 a    151 c    140 g     90 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 89;  Length 487;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    122 GCTCCACTTGCTCCA 108


RESULT   6
CNS01KVY/c
LOCUS       CNS01KVY      748 bp    DNA             STS       17-FEB-2000
DEFINITION  Anopheles gambiae STS SP6 end of clone 17P09 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            sequence tagged site.
ACCESSION   AL148863
VERSION     AL148863.1  GI:7007009
KEYWORDS    STS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 748)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .748
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                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="17P09"
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                     /note="end : SP6"
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c	11	13.8	92.0	1034	11	PT4G11A	M26253 Bacteriopha
c	12	13.8	92.0	1063	94	AF064721	AF064721 Mus muscu
c	13	13.8	92.0	1165	94	MUSIL2RGAM	D13821 Mouse mRNA
c	14	13.8	92.0	1187	93	HSA297692	AJ297692 Homo sapi
	15	13.8	92.0	1290	8	AF072549	AF072549 Danio rer
c	16	13.8	92.0	1394	94	AF047578	AF047578 Mus muscu
c	17	13.8	92.0	1410	58	AF250363	AF250363 Influenza
c	18	13.8	92.0	1410	58	AF250364	AF250364 Influenza
c	19	13.8	92.0	1429	94	BC004691	BC004691 Mus muscu
c	20	13.8	92.0	1438	59	IAU86144	U86144 Influenza A
c	21	13.8	92.0	1438	59	IAU86145	U86145 Influenza A
c	22	13.8	92.0	1458	58	FLAHANENJ8	M27970 Influenza v
c	23	13.8	92.0	1458	58	FLANANJ76	D31946 Influenza A
c	24	13.8	92.0	1458	59	IAU53166	U53166 Influenza A
c	25	13.8	92.0	1590	94	MUSIL2RGA	D13565 Mus musculu
c	26	13.8	92.0	1608	9	AR072026	AR072026 Sequence
c	27	13.8	92.0	1608	94	MUSIL2RG	L20048 Mouse inter
c	28	13.8	92.0	1623	94	MMMI2RGC	X75337 M.musculus
c	29	13.8	92.0	1649	11	MYT4G12	X06792 Bacteriopha
	30	13.8	92.0	1855	7	AF056218	AF056218 Bos tauru
c	31	13.8	92.0	2044	5	AF077299	AF077299 Drosophil
c	32	13.8	92.0	2100	93	HSIL12R	U03187 Human IL12
c	33	13.8	92.0	2104	9	AR052275	AR052275 Sequence
c	34	13.8	92.0	2104	9	AR059955	AR059955 Sequence
c	35	13.8	92.0	2104	9	AR068104	AR068104 Sequence
c	36	13.8	92.0	2104	10	I23702	I23702 Sequence 1
c	37	13.8	92.0	2117	9	A68598	A68598 Sequence 12
c	38	13.8	92.0	2117	9	A79383	A79383 Sequence 12
c	39	13.8	92.0	2196	12	AF056026	AF056026 Arabidops
c	40	13.8	92.0	2232	10	E31424	E31424 Gene partic
c	41	13.8	92.0	2232	12	AF093241	AF093241 Arabidops
c	42	13.8	92.0	2270	93	HSM801945	AL137281 Homo sapi
c	43	13.8	92.0	2300	9	AR097221	AR097221 Sequence
c	44	13.8	92.0	2309	12	AF086906	AF086906 Arabidops
c	45	13.8	92.0	2431	8	XLFYNR	X52188 Xenopus fyn

ALIGNMENTS

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RESULT   1
AR039961/c
LOCUS       AR039961       17 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 809 from patent US 5807743.
ACCESSION   AR039961
VERSION     AR039961.1  GI:5959324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE     Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL   Patent: US 5807743-A 809 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
BASE COUNT        6 a      1 c      7 g      3 t
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 9;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     17 GCTCCATTTACTCCA 3


RESULT   2
```

```
MUSAIC2B10/c
LOCUS       MUSAIC2B10    160 bp    DNA             ROD       27-APR-1993
DEFINITION  Mus musculus IL-3, IL-5, and GM-CSF receptor B-subunit (AIC2B)
            gene, exon 10.
ACCESSION   M95509
VERSION     M95509.1  GI:191832
KEYWORDS    GM-CSF receptor B-subunit; IL-3 receptor B-subunit; IL-5 receptor
            B-subunit.
SEGMENT     10 of 14
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 160)
  AUTHORS   Gorman,D.M., Itoh,N., Jenkins,N.A., Gilbert,D.A., Copeland,N.G. and
            Miyajima,A.
  TITLE     Chromosomal localization and organization of the murine genes
            encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3,
            granulocyte/macrophage colony-stimulating factor, and interleukin 5
            receptors
  JOURNAL   J. Biol. Chem. 267, 15842-15848 (1992)
  MEDLINE   92348451
FEATURES             Location/Qualifiers
     source          1. .160
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
     exon            1. .160
                     /gene="AIC2B"
                     /number=10
BASE COUNT       46 a     42 c     47 g     25 t
ORIGIN


  Query Match           92.0%;  Score 13.8;  DB 94;  Length 160;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    132 GCTCCACTTGCTCCA 118


RESULT   3
S75844S5/c
LOCUS       S75844S5      179 bp    DNA             ROD       15-JUN-1995
DEFINITION  IL-2R gamma =interleukin-2 receptor gamma chain [mice, BALB/c,
            liver, Genomic, 179 nt, segment 5 of 8].
ACCESSION   S75849
VERSION     S75849.1  GI:861551
KEYWORDS    .
SEGMENT     5 of 8
SOURCE      Mus sp. liver BALB/c.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 179)
  AUTHORS   DiSanto,J.P., Certain,S., Wilson,A., MacDonald,H.R., Avner,P.,
            Fischer,A. and de Saint Basile,G.
  TITLE     The murine interleukin-2 receptor gamma chain gene: organization,
            chromosomal localization and expression in the adult thymus
  JOURNAL   Eur. J. Immunol. 24 (12), 3014-3018 (1994)
  MEDLINE   95104285
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 161704] from the original journal article.
            This sequence comes from Fig. 2 and 3.
            Map location: X region 40.
FEATURES             Location/Qualifiers
     source          1. .179
                     /organism="Mus sp."
                     /db_xref="taxon:10095"
BASE COUNT       48 a     37 c     50 g     44 t
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:52:01 ; Search time 1774.1 Seconds
(without alignments)
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Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAYTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	13.8	92.0	17	9	AR039961	AR039961 Sequence
c 2	13.8	92.0	160	94	MUSAIC2B10	M95509 Mus musculu
c 3	13.8	92.0	179	95	S75844S5	S75849 IL-2R gamma
c 4	13.8	92.0	271	6	LAU72036	U72036 Leptothorax
c 5	13.8	92.0	487	89	AF227552	AF227552 Macaca mu
c 6	13.8	92.0	748	53	CNS01KVY	AL148863 Anopheles
c 7	13.8	92.0	783	9	AX053546	AX053546 Sequence
8	13.8	92.0	900	53	CNS01EI0	AL140569 Anopheles

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PR   31-MAY-1994;   94US-0248532.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chizzonite RA,  Chua AO,  Gubler UA,  Truitt TP;
XX
DR   WPI; 1995-076349/11.
DR   P-PSDB; AAR69632.
XX
PT   DNA encoding a low affinity interleukin-12 receptor - used to
PT   bind or scavenge IL-12 to cause immune suppression, e.g. to
PT   suppress graft-vs-host reaction, allograft rejection or
PT   inflammation, and to treat autoimmune conditions
XX
PS   Claim 3; Page 24-27; 61pp; English.
XX
CC   A cDNA library of PHA-activated peripheral blood mononuclear cells
CC   in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor
CC   cDNAs by panning.  An isolated cDNA was sequenced (AAQ83844); it
CC   encoded a 662-amino acid low affinity IL-12 receptor (AAR69632).
CC   Recombinant IL-12 receptor was expressed in COS cells, and can be
CC   used for therapeutic or diagnostic purposes.
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SQ   Sequence 2104 BP; 411 A; 624 C; 658 G; 411 T; 0 other;


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Job time: 7426 sec
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RESULT 15
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AC AAQ83844;
XX
DT 05-SEP-1995 (first entry)
XX
DE Human interleukin-12 receptor cDNA.
XX
KW Interleukin-12 receptor; IL-12; immune suppression;
KW immunosuppressive; graft-versus-host reaction; allograft rejection;
KW inflammation; autoimmune disease; ds.
XX
OS Homo sapiens.

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Db    891 GCTCCACTTACTCCA 877


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ID   AAQ71977 standard; DNA; 1608 BP.
XX
AC   AAQ71977;
XX
DT   03-MAY-1995  (first entry)
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DE   Murine IL-2R gamma gene.
XX
KW   Murine IL2-R gamma; X-linked severe combined immunodeficiency;
KW   XSCID; interleukin; ss.
XX
OS   Mus musculus.
XX
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XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Leonard WJ,  Mcbride WO,  Noguchi M;
XX
DR   WPI; 1994-303046/37.
DR   P-PSDB; AAR59094.
XX
PT   Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
PT   comprises detecting mutated IL-2R gamma gene, also vectors and
PT   transgenic animals containing the mutated gene
XX
PS   Example 1; Fig 7; 98pp; English.
XX
CC   AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094,
CC   this was used in the development of a claimed method for the
CC   diagnosis of X-linked severe combined immunodeficiency (XSCID),
CC   in female carriers and male sufferers.
XX
SQ   Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;


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Db     750 GCTCCATTTACTCCA 736


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AC   AAC46177;
XX
DT   18-OCT-2000  (first entry)
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DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 49177.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
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OS   Arabidopsis thaliana.
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PN   EP1033405-A2.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 92.0%; Score 13.8; DB 21; Length 1537;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||

```
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db     803 GCTCCACTTACTCCA 789


RESULT  11
AAV26248/c
ID   AAV26248 standard; DNA; 1414 BP.
XX
AC   AAV26248;
XX
DT   24-JUL-1998  (first entry)
XX
DE   Genomic DNA SEQ ID NO:228 from WO9804684 encoding SEQ ID NO:229.
XX
KW   Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
KW   pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
KW   Dirofilaria immitis; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1414
FT                   /*tag= a
FT                   /note= "encodes protein given in AAW55998; a stop codon
FT                          is given in between amino acids at the end of
FT                          the protein"
XX
PN   WO9804684-A1.
XX
PD   05-FEB-1998.
XX
PF   25-JUL-1997;   97WO-US12212.
XX
PR   25-JUL-1996;   96US-0686968.
XX
PA   (SYTR ) SYNTRO CORP.
XX
PI   Cochran MD,  Junker DE;
XX
DR   WPI; 1998-130677/12.
DR   P-PSDB; AAW55998.
XX
PT   Recombinant swine pox virus - useful in vaccine for immunising
PT   animal against swine pox virus
XX
PS   Disclosure; Page 402-405; 473pp; English.
XX
CC   The present sequence represents SEQ ID NO:228 from the present invention,
CC   this sequence is only given in the sequence listing and is not mentioned
CC   further in the specification. The present invention specifically
CC   describes recombinant swinepox virus (SPV) comprising a foreign DNA (I)
CC   inserted into a SPV CC   genome which is capable of being expressed in a
CC   host cell into which the virus is introduced, where (I) is inserted into:
CC   (a) an EcoRI site within a region corresponding to a 3.2 kb subfragment
CC   of the HindIII K fragment which contains both a HindIII and an EcoRI
CC   site, of the SPV genome, and optionally (b) an AccI site within a region
CC   corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M
CC   fragment. The recombinant SPV can be used in a vaccine for immunising an
CC   animal against SPV. The invention also provides a method for testing a
CC   swine to determine whether the swine has been vaccinated with the
CC   vaccine, particularly containing S-SPV-008, or is infected with a
CC   naturally occurring wild-type pseudorabies virus. Also (I) inserted into
CC   recombinant SPV can be used in a diagnostic assay, e.g. Feline
CC   immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis
CC   p39 and 22kd are useful to detect feline immunodeficiency caused by FIV
CC   and to detect heartworm caused by D. immitis respectively.
XX
SQ   Sequence 1414 BP; 463 A; 253 C; 324 G; 374 T; 0 other;

  Query Match             92.0%;  Score 13.8;  DB 19;  Length 1414;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db    1037 ACTCCATTTGCTCCA 1023


RESULT  12
AAC36394/c
ID   AAC36394 standard; DNA; 1537 BP.
XX
AC   AAC36394;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 13639.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
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PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 92.0%; Score 13.8; DB 21; Length 1290;

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Qy      1 RCTCCAYTTRCTCCA 15
            :|||||:||:|||||
Db     98 GCTCCATTTGCTCCA 84


RESULT  9
AAZ24836/c
ID   AAZ24836 standard; DNA; 1217 BP.
XX
AC   AAZ24836;
XX
DT   02-DEC-1999  (first entry)
XX
DE   Human secreted protein gene 26 clone HPMFP40.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9947540-A1.
XX
PD   23-SEP-1999.
XX
PF   18-MAR-1999;   99WO-US05804.
XX
PR   19-MAR-1998;   98US-0078563.
PR   19-MAR-1998;   98US-0078566.
PR   19-MAR-1998;   98US-0078573.
PR   19-MAR-1998;   98US-0078574.
PR   19-MAR-1998;   98US-0078576.
PR   19-MAR-1998;   98US-0078577.
PR   19-MAR-1998;   98US-0078578.
PR   19-MAR-1998;   98US-0078579.
PR   19-MAR-1998;   98US-0078581.
PR   01-APR-1998;   98US-0080312.
PR   01-APR-1998;   98US-0080313.
PR   01-APR-1998;   98US-0080314.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Rosen CA,  Yu G,  Young PE,  Feng P,  Soppet DR;
PI   Wei Y,  Endress GA,  Duan RD,  Kyaw H,  Ebner R,  Lafleur DW;
PI   Olsen HS,  Shi Y,  Moore PA;
XX
DR   WPI; 1999-562050/47.
DR   P-PSDB; AAY41333.
XX
PT   New isolated human genes, useful for diagnosis and treatment of e.g.
PT   cancers, neurological disorders, immune diseases, inflammation or blood
PT   disorders -
XX
PS   Claim 1; Page 314; 484pp; English.
XX
CC   This sequence represents a nucleic acid molecule which encodes a
CC   secreted human protein.  The gene number, and the clone it is derived
CC   from, are detailed in the descriptor line.  The gene can be used to
CC   generate fusion proteins by linking to the gene to a human immunoglobulin
CC   Fc portion (e.g. AAZ24802) for increasing the stability of the fused
CC   protein as compared to the human protein only.
CC   The invention relates to 95 novel genes and their fragments (nucleic
CC   acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404)
CC   which are useful for preventing, treating or ameliorating  medical
CC   conditions e.g. by protein or gene therapy.  Also, pathological
CC   conditions can be diagnosed by determining the amount of the new
CC   polypeptides in a sample or by determining the presence of mutations in
CC   the new polynucleotides. Specific uses are described for each of the 95
CC   polynucleotides, based on which tissues they are most highly expressed in
CC   (see AAZ24811 for described uses).
XX
SQ   Sequence 1217 BP; 346 A; 232 C; 223 G; 416 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 20;  Length 1217;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
            :|||||:||:|||||
Db   1076 ACTCCACTTGCTCCA 1062


RESULT  10
AAC48659/c
ID   AAC48659 standard; DNA; 1290 BP.
XX
AC   AAC48659;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 58287.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
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PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
```

```
CC   allergy and other inflammatory conditions. The ribozymes are also used
CC   to induce tolerance in a recipient to alloantigen from a donor.
XX
SQ   Sequence 17 BP; 6 A; 1 C; 7 G; 3 U; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 19;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     17 GCTCCATTTACTCCA 3


RESULT   7
AAA89732/c
ID   AAA89732 standard; cDNA; 494 BP.
XX
AC   AAA89732;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Mouse IL-3 receptor nucleotide sequence #3.
XX
KW   Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
KW   antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant;
KW   vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW   digestion disorder; wound healing disorder; gene therapy; ss.
XX
OS   Mus sp.
XX
PN   WO200043419-A2.
XX
PD   27-JUL-2000.
XX
PF   20-JAN-2000; 2000WO-US01431.
XX
PR   20-JAN-1999;   99US-0116534.
PR   26-JAN-1999;   99US-0117274.
PR   26-JAN-1999;   99US-0117308.
PR   26-JAN-1999;   99US-0117309.
PR   26-JAN-1999;   99US-0117312.
PR   01-FEB-1999;   99US-0118177.
PR   01-FEB-1999;   99US-0118178.
PR   01-FEB-1999;   99US-0118179.
PR   09-FEB-1999;   99US-0119286.
PR   11-FEB-1999;   99US-0119998.
PR   11-FEB-1999;   99US-0119759.
XX
PA   (RIGE-) RIGEL PHARM INC.
XX
PI   Luo Y;
XX
DR   WPI; 2000-482908/42.
XX
PT   New nucleic acids encoding Exo proteins which are useful in the
PT   diagnosis, treatment or prevention of exocytosis-mediated disorders
PT   such as asthma, inflammation and allergies -
XX
PS   Disclosure; Page 302-303; 305pp; English.
XX
CC   The present sequence encodes a polypeptide which is associated with
CC   the exocytosis pathway. cDNA molecules encoding proteins involved in
CC   exocytosis have been isolated by yeast one-hybrid and two-hybrid
CC   screening. Novel proteins, termed Exo proteins, have been identified that
CC   interact with known exocytosis-associated proteins such as GS27, alpha
CC   snap, unc18-1, vamp3, snap-23, and the rab family of proteins.
CC   Exo proteins and their agonists and antagonists are useful in the
CC   diagnosis, treatment or prevention of exocytosis-mediated disorders
CC   such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
CC   (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC   diabetes, digestion disorders and wound healing disorders.
CC   The nucleic acids, antagonists or agonists of Exo proteins are useful
CC   in gene therapy. The nucleic acids are also useful for generating
CC   transgenic or knock-out animals which can be used in the
CC   development and screening of therapeutically useful reagents.
XX
SQ   Sequence 494 BP; 125 A; 135 C; 129 G; 101 T; 4 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 494;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    231 GCTCCACTTGCTCCA 217


RESULT   8
AAF22733/c
ID   AAF22733 standard; cDNA; 783 BP.
XX
AC   AAF22733;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human gastric cancer associated antigen nucleotide sequence SEQ ID:312.
XX
KW   Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW   cancer associated antigen; cytostatic; cancer vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073801-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14749.
XX
PR   28-MAY-1999;   99US-0136526.
PR   10-SEP-1999;   99US-0153454.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Obata Y;
XX
DR   WPI; 2001-025274/03.
XX
PT   Nucleic acids  encoding breast, gastric and prostate cancer associated
PT   antigen precursors, useful for diagnosing and treating a condition
PT   characterized by expression of an abnormal amount of a protein, e.g.
PT   cancer -
XX
PS   Claim 50; Page 375-376; 799pp; English.
XX
CC   AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC   represent nucleotide sequences encoding human breast, gastric and
CC   prostate cancer associated antigen precursors (CAAP) respectively.
CC   AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC   represent human breast, gastric and prostate CAAP protein sequence
CC   respectively. CAAPs have cytostatic activity and can be used in the
CC   production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC   acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC   condition characterised by expression of an abnormal amount of a protein,
CC   e.g. cancer.
XX
SQ   Sequence 783 BP; 255 A; 147 C; 160 G; 216 T; 5 other;


  Query Match             92.0%;  Score 13.8;  DB 22;  Length 783;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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```
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 44; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 5 A; 1 C; 6 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db      15 GCTCCATTTACTCCA 1


RESULT   5
AAZ90914/c
ID   AAZ90914 standard; DNA; 15 BP.
XX
AC   AAZ90914;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #142.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 45; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db      15 ACTCCACTTGCTCCA 1


RESULT   6
AAV94975/c
ID   AAV94975 standard; RNA; 17 BP.
XX
AC   AAV94975;
XX
DT   24-FEB-1999  (first entry)
XX
DE   Mouse IL-2 receptor g-chain substrate position 725.
XX
KW   Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW   hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW   autoimmune disease; psoriasis; allergy; inflammatory disease;
KW   graft rejection; ss.
XX
OS   Mus sp.
XX
PN   WO9824913-A2.
XX
PD   11-JUN-1998.
XX
PF   02-DEC-1997;   97WO-US21748.
XX
PR   03-DEC-1996;   96US-0758306.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   McSwiggen JA,  Stinchcomb DT;
XX
DR   WPI; 1998-333332/29.
XX
PT   Ribozymes targeted to interleukin 2 - useful for treating e.g.
PT   cancer, autoimmune disease and allergies
XX
PS   Claim 4; Page 42; 61pp; English.
XX
CC   The present sequence invention describes ribozymes targeted to modulate
CC   the synthesis and/or expression of interleukin (IL)-2R gamma encoded
CC   RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC   AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC   from the present invention. The ribozymes can be used for the treatment
CC   of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,
```

```
PS   Claim 12; Page 52; 87pp; English.
XX
CC   5 Degenerate hybridisation probes (AAT17870-74) are based on a
CC   conserved motif (AAR92812) found in haemopoietin receptors.  The
CC   probes are used in the identification and/or cloning of genes
CC   coding for novel haemopoietin receptors, e.g. the murine
CC   interleukin-11 (IL-11) receptor alpha chain gene (AAT17868).  Such
CC   receptors are defined by their ability to hybridise to the
CC   probes under medium stringency conditions.
XX
SQ   Sequence 15 BP; 2 A; 6 C; 0 G; 4 T; 3 other;


  Query Match             92.0%;  Score 13.8;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          ||||||||||||||||
Db      1 rctccayttrctcca 15


RESULT   2
AAZ90859/c
ID   AAZ90859 standard; DNA; 15 BP.
XX
AC   AAZ90859;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #87.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 42; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 5 A; 1 C; 6 G; 3 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     15 ACTCCATTTGCTCCA 1


RESULT   3
AAZ90874/c
ID   AAZ90874 standard; DNA; 15 BP.
XX
AC   AAZ90874;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #102.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP03351.
XX
PR   24-JUN-1998;   98JP-0214720.
PR   19-OCT-1998;   98JP-0297409.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders -
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family
CC   sequences were initially searched for comparison on a nucleic acid
CC   database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC   the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC   AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
CC   sequences used in the search. Antibodies to the NR8 family proteins are
CC   used for the diagnosis of blood formation disorders. Compounds identified
CC   as binding to the proteins are used for the treatment of such disorders.
XX
SQ   Sequence 15 BP; 5 A; 0 C; 6 G; 4 T; 0 other;


  Query Match             92.0%;  Score 13.8;  DB 21;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     15 ACTCCATTTACTCCA 1


RESULT   4
AAZ90907/c
ID   AAZ90907 standard; DNA; 15 BP.
XX
AC   AAZ90907;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #135.
XX
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:43 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAYTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13.8	92.0	15	17	AAT17874	Haemopoietin recep
c 2		13.8	92.0	15	21	AAZ90859	Human NR8 gene pro
c 3		13.8	92.0	15	21	AAZ90874	Human NR8 gene pro
c 4		13.8	92.0	15	21	AAZ90907	Human NR8 gene pro
c 5		13.8	92.0	15	21	AAZ90914	Human NR8 gene pro
c 6		13.8	92.0	17	19	AAV94975	Mouse IL-2 recepto
c 7		13.8	92.0	494	21	AAA89732	Mouse IL-3 recepto
c 8		13.8	92.0	783	22	AAF22733	Human gastric canc
c 9		13.8	92.0	1217	20	AAZ24836	Human secreted pro
c 10		13.8	92.0	1290	21	AAC48659	Arabidopsis thalia
c 11		13.8	92.0	1414	19	AAV26248	Genomic DNA SEQ ID
c 12		13.8	92.0	1537	21	AAC36394	Arabidopsis thalia
c 13		13.8	92.0	1608	15	AAQ71977	Murine IL-2R gamma
c 14		13.8	92.0	2061	21	AAC46177	Arabidopsis thalia
c 15		13.8	92.0	2104	16	AAQ83844	Human interleukin-
c 16		13.8	92.0	2104	18	AAT59732	Human interleukin-
c 17		13.8	92.0	2104	21	AAA11001	Human interleukin
c 18		13.8	92.0	2117	19	AAV16362	cDNA sequence of t
c 19		13.8	92.0	2204	21	AAZ29279	A. thaliana Ethyle
c 20		13.8	92.0	2232	21	AAZ57348	Gravitropism stimu
c 21		13.8	92.0	2299	17	AAT11640	Murine osteogenic
c 22		13.8	92.0	2300	21	AAA59898	Murine DNA sequenc
c 23		13.8	92.0	2408	21	AAZ52490	Human secreted pro
c 24		13.8	92.0	3182	13	AAQ25799	hLIF-R. Homo sapi
c 25		13.8	92.0	3182	14	AAQ42590	Human LIF-R N-term
c 26		13.8	92.0	3182	15	AAQ58425	Human LIF-R clone
c 27		13.8	92.0	3182	15	AAQ55940	Human leukaemia in
c 28		13.8	92.0	3591	15	AAQ58427	Human LIF-R. Homo
c 29		13.8	92.0	3591	15	AAQ55942	Human leukaemia in
c 30		13.8	92.0	3591	16	AAQ92272	Human leukaemia in
c 31		13.8	92.0	3980	21	AAZ57349	Gravitropism stimu
c 32		13.8	92.0	7072	21	AAZ29278	A. thaliana Ethyle
c 33		13.2	88.0	15	19	AAV49499	WSXWS degenerate p
c 34		13.2	88.0	30	22	AAF76707	Human PTP PEST cod
35		13.2	88.0	50	21	AAZ47151	Liposome membrane-
36		13.2	88.0	194	21	AAA41744	Human secreted exp
c 37		13.2	88.0	436	21	AAC01348	Human secreted pro
c 38		13.2	88.0	480	21	AAC01349	Human secreted pro
c 39		13.2	88.0	618	21	AAC43764	Zea mays DNA fragm
c 40		13.2	88.0	762	21	AAA26722	Candida albicans p
c 41		13.2	88.0	1485	21	AAC42934	Arabidopsis thalia
42		13.2	88.0	1569	21	AAC36662	Arabidopsis thalia
43		13.2	88.0	151826	21	AAF22291	BAC containing rep
c 44		12.8	85.3	17	19	AAT94135	Probe 9560 for hae
45		12.8	85.3	30	20	AAX87693	Human TPST-1 cDNA

ALIGNMENTS

RESULT 1
AAT17874
ID AAT17874 standard; DNA; 15 BP.
XX
AC AAT17874;
XX
DT 21-MAY-1996 (first entry)
XX
DE Haemopoietin receptor probe HYB5.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN WO9607737-A1.
XX
PD 14-MAR-1996.
XX
PF 05-SEP-1995; 95WO-AU00578.
XX
PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ;
XX
DR WPI; 1996-171612/17.
XX
PT Nucleic acid encoding haemopoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists
XX

```
           ,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N., Hawkins,T.,
           Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston
           ,J.
  TITLE    A survey of expressed genes in Caenorhabditis elegans
  JOURNAL  Nature Genet. 1, 114-123 (1992)
  MEDLINE  93250982
COMMENT    Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
           (USA) Dept. of Genetics or (UK)
           (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
           Molecular Biology
           Box 8232,4566 Scott Ave.,St. Louis,MI 63110,USA,or,Hills Road
           ,Cambridge CB2 2QH,UK
           Tel: (USA) (314)3627072 or (UK) (0223)248011
           Fax: (USA) (314)3624137 or (UK) (0223)402008
           Email: rw@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
           single read.
FEATURES             Location/Qualifiers
     source          1. .324
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                     /strain="Bristol N2"
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                     /lab_host="MC1061"
                     /note="Vector: lambdaphage SHLX2; Mixed stage
                     hermaphrodite cDNA library. Partially normalized by
                     successively picking groups of clones that didn't
                     hybridize to previously picked clones. Vector: lambdaphage
                     SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host:
                     MC1061"
BASE COUNT       96 a     54 c     89 g     77 t      8 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 159;  Length 324;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     80 GCTCCACTTGCTCCA 66


RESULT  15
BF936011/c
LOCUS       BF936011      324 bp    mRNA            EST       22-JAN-2001
DEFINITION  IL2-NT0198-291200-291-B05 NT0198 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF936011
VERSION     BF936011.1  GI:12353335
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-
            291200-291-B05&t3=2000-12-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 72.
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                     /clone_lib="NT0198"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       55 a     128 c     84 g     56 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 171;  Length 324;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     98 GCTCCATTTGCTCCA 84


Search completed: August 29, 2001, 19:22:20
Job time: 24143 sec
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contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI."
BASE COUNT 74 a 57 c 96 g 60 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 161; Length 287;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 150 ACTCCATTTGCTCCA 136

RESULT 12
B75501/c
LOCUS B75501 291 bp DNA GSS 08-APR-1999
DEFINITION RPCI11-16K9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16K9, DNA sequence.
ACCESSION B75501
VERSION B75501.1 GI:2771188
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 291)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI11-16K9.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .291
/organism="Homo sapiens"
/db_xref="GDB:7506008"
/db_xref="taxon:9606"
/clone="RPCI-11-16K9"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 76 a 70 c 95 g 50 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 256; Length 291;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 65 GCTCCACTTGCTCCA 51

RESULT 13
B40700
LOCUS B40700 305 bp DNA GSS 18-OCT-1997
DEFINITION HS-1052-A1-E09-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=17 Row=I, DNA sequence.
ACCESSION B40700
VERSION B40700.1 GI:2544952
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 305)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 774 row: I column: 17
Class: BAC ends
High quality sequence stop: 305.
FEATURES Location/Qualifiers
source 1. .305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=CT 774 Col=17 Row=I"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 76 a 63 c 62 g 104 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 256; Length 305;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 260 ACTCCATTTACTCCA 274

RESULT 14
M89352/c
LOCUS M89352 324 bp mRNA EST 16-SEP-1992
DEFINITION CEL21F10 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm21f10 5', mRNA sequence.
ACCESSION M89352
VERSION M89352.1 GI:275857
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 324)
AUTHORS Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 272)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M. , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y. , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y. , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I. , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino ,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .272
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C530024L16"
/clone_lib="RIKEN full-length enriched, 12 days embryo spinal cord"
/tissue_type="spinal cord"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 72 a 62 c 61 g 77 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 133; Length 272;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 3 ACTCCACTTGCTCCA 17

RESULT 11
BB585089/c
LOCUS BB585089 287 bp mRNA EST 30-NOV-2000
DEFINITION BB585089 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430004A04 5', mRNA sequence.
ACCESSION BB585089
VERSION BB585089.1 GI:11481633
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 287)
AUTHORS Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P. , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .287
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9430004A04"
/clone_lib="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"
/tissue_type="embryonic body between diaphragm region and neck"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

Lambda ZAP II cDNA library was constructed from mRNA extracted from etiolated leaf tissue of the rice cultivar 'IR36' and converted to pBluescript (amp resistant) as described in Causse et al. (1994) Genetics 138:1251-1274. For insert amplification, Use M13 forward and reverse primers. Clones from this library are designated with the prefix 'RZ'."
BASE COUNT 89 a 45 c 47 g 48 t 2 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 4; Length 231;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 144 ACTCCACTTACTCCA 158

RESULT 8
C42038
LOCUS C42038 240 bp mRNA EST 18-OCT-1999
DEFINITION C42038 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk284c9 5', mRNA sequence.
ACCESSION C42038
VERSION C42038.1 GI:2378275
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 240)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano ,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .240
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk284c9"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 73 a 56 c 50 g 57 t 4 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 156; Length 240;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 167 GCTCCACTTGCTCCA 181

RESULT 9
AI119961/c
LOCUS AI119961 248 bp mRNA EST 02-SEP-1998
DEFINITION uc23c06.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1398826 5' similar to gb:D13565 Mouse mRNA for interleukin 2 receptor gamma chain (MOUSE);, mRNA sequence.
ACCESSION AI119961
VERSION AI119961.1 GI:3520285
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 248)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:910542
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .248
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1398826"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 74 a 51 c 68 g 55 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 16; Length 248;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:||:|||||
Db 214 GCTCCATTTACTCCA 200

RESULT 10
BB420958
LOCUS BB420958 272 bp mRNA EST 16-JUL-2000
DEFINITION BB420958 RIKEN full-length enriched, 12 days embryo spinal cord Mus musculus cDNA clone C530024L16 3', mRNA sequence.
ACCESSION BB420958
VERSION BB420958.1 GI:9242313
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

```
RESULT   5
CNS032CC/c
LOCUS       CNS032CC      215 bp    DNA             GSS       15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            206N11 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL224661
VERSION     AL224661.1  GI:7883532
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 215)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 215)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 215)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .215
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="206N11"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG206CG06SP1~end :
                     PUC-Ori"
BASE COUNT       46 a     58 c     63 g     43 t      5 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 220;  Length 215;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db     169 GCTCCACTTGCTCCA 155


RESULT   6
R74725/c
LOCUS       R74725        216 bp    mRNA            EST       25-JUL-1996
DEFINITION  MDB0891R Mouse brain, Stratagene Mus musculus cDNA 5'end, mRNA
            sequence.
ACCESSION   R74725
VERSION     R74725.1  GI:849928
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 216)
  AUTHORS   Beier,D. and Brady,K.
  TITLE     Mouse brain cDNAs
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Sikela JM
            Department of Pharmacology
            University of Colorado Health Sciences Center
            Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
            Tel: 3032708637
            Fax: 3032707097
            Email: nikki@tally.uchsc.edu
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .216
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone_lib="Mouse brain, Stratagene"
                     /lab_host="E. coli XL1-Blue"
                     /note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
                     The mouse brain library (Stratagene    ) was constructed by
                     oligo-(dT) priming and directional cloning in Uni-ZAP XR
                     phage using whole brain mRNA from a Balb C post natal 20
                     day."
BASE COUNT       45 a     54 c     61 g     55 t      1 others
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 188;  Length 216;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db     104 ACTCCACTTGCTCCA 90


RESULT   7
AA231776
LOCUS       AA231776      231 bp    mRNA            EST       15-SEP-2000
DEFINITION  RZ612.F cDNA from rice Oryza sativa cDNA clone RZ612, mRNA
            sequence.
ACCESSION   AA231776
VERSION     AA231776.1  GI:1854148
KEYWORDS    EST.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 231)
  AUTHORS   VanDeynze,A.E., Sorrells,M.E., Park,W.D., Ayres,N.M., Fu,H.,
            Cartinhour,S.W., Paul,E. and McCouch,S.R.
  TITLE     Anchor Probes for Comparative Mapping of Grass Genera
  JOURNAL   Theor. Appl. Genet. 97, 356-369 (1998)
COMMENT     Contact: McCouch SR
            Dept Plant Breeding
            Cornell University
            Ithaca, NY 14853-1901, USA
            Tel: 607 255 0420
            Fax: 607 255 6683
            Email: srm4@cornell.edu
            cDNA from rice (Oryza sativa); forward sequence of RFLP probe
            RZ612. Sequence determined by Nicola M. Ayres. For mapping
            information, additional citations and other related information
            concerning this probe, please refer to the RiceGenes database at
            http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes&
            class=Marker&object=RZ612.
FEATURES             Location/Qualifiers
     source          1. .231
                     /organism="Oryza sativa"
                     /cultivar="IR36"
                     /db_xref="RiceGenes:RZ612"
                     /db_xref="taxon:4530"
                     /clone="RZ612"
                     /clone_lib="cDNA from rice"
                     /note="Vector: Lambda ZAP II/pBluescript; Site_1: EcoRI; A
```

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          High quality sequence start: 9
          High quality sequence stop: 125
          POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .154
                     /organism="Sorghum bicolor"
                     /db_xref="taxon:4558"
                     /clone_lib="Ovary 2 (OV2)"
                     /note="Organ: Mix of ovaries of varying immature stages
                     from 8-week-old plants; Vector: pBluescript II from Lambda
                     Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
                     from poly-A RNA in the cloning vector lambda ZAP II.
                     Clones to be sequenced were prepared by mass excision."
BASE COUNT       48 a     27 c     33 g     46 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 174;  Length 154;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    129 GCTCCATTTGCTCCA 115


RESULT   3
AQ554938/c
LOCUS       AQ554938      186 bp    DNA             GSS       28-MAY-1999
DEFINITION  RPCI-11-366P19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-366P19
            , DNA sequence.
ACCESSION   AQ554938
VERSION     AQ554938.1  GI:4914115
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 186)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .186
                     /organism="Homo sapiens"
                     /db_xref="GDB:7640538"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-366P19"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT       44 a     43 c     64 g     35 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 230;  Length 186;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db     54 GCTCCACTTGCTCCA 40


RESULT   4
BE171588
LOCUS       BE171588      192 bp    mRNA            EST       21-JUN-2000
DEFINITION  CM0-HT0548-210200-233-e07 HT0548 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE171588
VERSION     BE171588.1  GI:8634223
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 192)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM0-HT0548-210
            200-233-e07&t3=2000-02-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 2
            High quality sequence stop: 192.
FEATURES             Location/Qualifiers
     source          1. .192
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0548"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       34 a     60 c     37 g     61 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 164;  Length 192;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RCTCCAYTTRCTCCA 15
          :|||||:||:|||||
Db    107 GCTCCACTTGCTCCA 121
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.8	92.0	147	1	AA038484	AA038484 mi83c09.r
c 2	13.8	92.0	154	174	BG159502	BG159502 OV2_5_B09
c 3	13.8	92.0	186	230	AQ554938	AQ554938 RPCI-11-3
4	13.8	92.0	192	164	BE171588	BE171588 CM0-HT054
c 5	13.8	92.0	215	220	CNS032CC	AL224661 Tetraodon
c 6	13.8	92.0	216	188	R74725	R74725 MDB0891R Mo
7	13.8	92.0	231	4	AA231776	AA231776 RZ612.F c
8	13.8	92.0	240	156	C42038	C42038 C42038 Yuji
c 9	13.8	92.0	248	16	AI119961	AI119961 uc23c06.r
10	13.8	92.0	272	133	BB420958	BB420958 BB420958
c 11	13.8	92.0	287	161	BB585089	BB585089 BB585089
c 12	13.8	92.0	291	256	B75501	B75501 RPCI11-16K9
13	13.8	92.0	305	256	B40700	B40700 HS-1052-A1-
c 14	13.8	92.0	324	159	M89352	M89352 CEL21F10 Ch
c 15	13.8	92.0	324	171	BF936011	BF936011 IL2-NT019
c 16	13.8	92.0	328	138	BE650167	BE650167 UI-M-BH3-
c 17	13.8	92.0	341	190	W34848	W34848 mc62a03.r1
18	13.8	92.0	347	169	BF814907	BF814907 IL5-CI014
19	13.8	92.0	350	240	AZ238189	AZ238189 RPCI-23-7
c 20	13.8	92.0	360	26	AV185887	AV185887 AV185887
c 21	13.8	92.0	360	26	AV192824	AV192824 AV192824
c 22	13.8	92.0	360	26	AV194451	AV194451 AV194451
23	13.8	92.0	360	26	AV196133	AV196133 AV196133
24	13.8	92.0	360	156	C39835	C39835 C39835 Yuji
c 25	13.8	92.0	360	156	C42161	C42161 C42161 Yuji
c 26	13.8	92.0	360	156	C42410	C42410 C42410 Yuji
c 27	13.8	92.0	360	156	C43142	C43142 C43142 Yuji
c 28	13.8	92.0	360	156	C44203	C44203 C44203 Yuji
29	13.8	92.0	360	156	C47461	C47461 C47461 Yuji
c 30	13.8	92.0	360	156	C48718	C48718 C48718 Yuji
31	13.8	92.0	360	157	D67866	D67866 CELK087H7F
32	13.8	92.0	364	107	AU110033	AU110033 AU110033
33	13.8	92.0	370	17	AI215425	AI215425 qh11b10.x
c 34	13.8	92.0	371	156	C40410	C40410 C40410 Yuji
35	13.8	92.0	372	17	AI206294	AI206294 qr26f08.x
36	13.8	92.0	372	26	AV187143	AV187143 AV187143
c 37	13.8	92.0	372	156	C43783	C43783 C43783 Yuji
38	13.8	92.0	373	187	R38943	R38943 yd06f12.s1
39	13.8	92.0	374	187	R38942	R38942 yd06f11.s1
c 40	13.8	92.0	375	26	AV187242	AV187242 AV187242
41	13.8	92.0	375	26	AV193885	AV193885 AV193885
c 42	13.8	92.0	375	156	C47641	C47641 C47641 Yuji
c 43	13.8	92.0	375	156	C48090	C48090 C48090 Yuji
c 44	13.8	92.0	377	26	AV193301	AV193301 AV193301
45	13.8	92.0	377	156	D41868	D41868 RICS4820A R

ALIGNMENTS

```
RESULT   1
AA038484/c
LOCUS       AA038484      147 bp    mRNA            EST       28-AUG-1996
DEFINITION  mi83c09.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:473200 5', mRNA sequence.
ACCESSION   AA038484
VERSION     AA038484.1  GI:1513891
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 147)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:283944
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 130.
FEATURES             Location/Qualifiers
     source          1. .147
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:473200"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT       36 a     37 c     35 g     39 t
ORIGIN


  Query Match             92.0%;  Score 13.8;  DB 1;  Length 147;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RCTCCAYTTRCTCCA 15
           :|||||:||:|||||
Db     134 ACTCCACTTGCTCCA 120


RESULT   2
BG159502/c
LOCUS       BG159502      154 bp    mRNA            EST       06-FEB-2001
DEFINITION  OV2_5_B09.b1_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
            sequence.
ACCESSION   BG159502
VERSION     BG159502.1  GI:12693166
KEYWORDS    EST.
SOURCE      sorghum.
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 154)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
            ,L.H.
  TITLE     An EST database from Sorghum: ovaries of varying immature stages
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Cordonnier-Pratt MM
            Department of Botany
            The University of Georgia
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 542 1805
            Email: mmpratt@uga.edu
            Seq primer: JEN REV
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:17 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAYTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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